

GenCore version 5.1.6
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Om nucleic - nucleic search, using bw model

Run on: September 30, 2004, 19:57:17 ; Search time 4103.41 Seconds
(w/o alignments)
12684.514 Million cell updates/sec

Title: US-10-077-698-2

Perfect score: 1743

Sequence: tcgggactagttctagacgg.....aaaaaaaagggggg 1743

Scoring table: OLIGO_NUC

Gapop=60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing First 45 summaries

Database : BST:*

1: em_estha:*

2: em_esthun:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_p1n:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	582	33.4	936	14 CD517915	CD517915 AGENCOURT
2	508	29.1	611	12 BM739118	BM739118 K-BST008
3	393	22.5	1201	13 BX44304	BX44304
4	343	19.7	448	12 BM757151	BM757151 K-BST035

Tissue Procurement: Dr. Michael Brownstein
Email: cgbps-r@mail.nih.gov
CDNA Library preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNU)
DNA Sequencing by: AgenCourt Bioscience Corporation
Clone distribution: MGCC clone distribution information can be found through the I.M.A.G.E. Consortium/LNU at:

PRED. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
CDS17915
LOCUS CD517915 mRNA linear EST 06-JUN-2003
DEFINITION AGENCOURT 14364614 NIH MGCC_181 Homo sapiens cDNA clone IMAGE:3037270 5', mRNA sequence.
ACCESSION CDS17915
VERSION CDS17915.1 GI:31449633
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 936)
AUTHORS NIH-MGC http://mgcc.ncbi.nlm.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGCC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm1047 Bethesda, MD 20892

ALIGNMENTS

ALN469384 tm0Ba12.X
BF924587 IL0-NTO22
R4593 yg2e12.81
AW973354 ES1385497
AA558426 nk8bc09.s
BY506188 DKZP6560
BB061278 IL0-BT016
CD644362 AGENCOURT
CB448183 70224 MA
BC017579 Homo sapi
BUG660576 c165d10.z
AA421536 ziu0td09.r
A1584031 t8z2907.x
AQ192617 HS 2247.B
B052564 52729 Ma
BE005691 RC22-BN012
FO0574 HSB13C062.S
T7034 jc17a08.51
AW51652 xnb0d03.x
AA557984 n126h04.s
BG54763 60257508
AG103735 Pan trogl
CB270068 10089750.H
BF671675 60215134
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AU134346 DKP2547.P
BG323887 602242916
AU121388 AU121388
BX38149 BX381249
FO8214 HSC20C071.n
B64381 RPLC11-24D2
AB807579 nw66d04.s
AJ113765 nv8ze07.s
BG323887 602242916
FO8655 HSC1HC091.n
AQ195340 RP011-61
T40700 ya0bb06.81
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BU957861 AGENCOURT
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AZ694901 UP_523-17

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208	TTCAGGATGCTGCTCCGGCAACGTGCGGCCCTCTGTGCGTGGCGCCGGACAGCGC	267	Db
255	GCGGGCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	314	QY
268	GCGGGCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	327	Db
315	CTATCCCTGGGGCTGGCGCTGGACTGAGGCTGGCTGGCTGGCTGGGGGGCTTGCT	374	QY
328	CTATCCCTGGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT	387	Db
375	GCCACTCTGCTCTAGCTGATGACCTCTGGGGCTGAGCGGAGAGCTGACCTCTG	434	QY
388	GCCACTCTGCTCTAGCTGATGACCTCTGGGGCTGAGCGGAGAGCTGACCTCTG	447	Db
435	CGGTTAGCTGGAGGCGATGGTGTGATGACCTCTGGGGCTGAGCGGAGAGCTGAC	494	QY
448	CGGTTAGCTGGAGGCGATGGTGTGATGACCTCTGGGGCTGAGCGGAGAGCTGAC	507	Db
495	GGCGGG	554	QY
508	GG	567	Db
555	TGCCTCTCTGGGTTCTT	573	QY
568	TGCCTCTCTGGGTTCTT	586	Db
RESULT 3			
LOCUS	BX444304	1201 bp	mRNA
DEFINITION	Homo sapiens ADULT BRAIN Homo sapiens cDNA clone CSODN001YC21 5'-PRIME, mRNA sequence.	linear	EST 15-MAY-2003
ACCESSION	BX444304		
VERSION	BX444304.1	GI:30776199	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Li,W.B., Gruber,C., Jesse,J. and Polayes,D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Genoscope		
FEATURES	Genoscope - Centre National de Sequencage		
source	BP 191 91006 ERY cedex - France		
	Email: SeqPref@genoscope.cns.fr , Web : www.genoscope.cns.fr		
	Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 504.f, Contact : Feng Liang Email: filiang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope Sequence ID : CSODN001AB1QPI.		
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	/note="Organ: brain; Vector: pCMVSPORT-6; 1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRI sites of the pCMVSPORT-6 vector. Library was not normalized."		
ORIGIN			
Query Match	22.5%	Score 393;	DB 13; Length 1201;
Best Local Similarity	99.2%	Pred No. 9.8e-69;	
Matches	643;	Conservative 0;	Mismatches 5; Indels 0; Gaps 0;
RESULT 4			
LOCUS	BW757151	448 bp	mRNA
DEFINITION	K-BEST035924 S3SNU16 Homo sapiens cDNA clone S3SNU16-31-B04 5', mRNA sequence.	linear	EST 04-MAR-2002
ACCESSION	BW757151		
VERSION	BW757151.1	GI:19086766	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Kim,N.S., Hahn,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.		
TITLE	21C Frontier Korean EST Project 2001		
JOURNAL	Unpublished (2002)		
COMMENT	Contact: Kim YS		
	Genome Research Center		
	Korea Research Institute of Bioscience & Biotechnology		
	Korea Research Institute of Bioscience & Biotechnology		
	52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea		
	Tel : +82-42-860-4470		
	Fax : +82-42-860-4409		
	Email: yongsung@mail.kribb.re.kr		
	Plate: 31 row: B column: 04		
	High quality sequence stop: 448.		

JOURNAL		PROC. NATL. ACADEM. SCI. U.S.A. 97 (7), 3491-3496 (2000)	
COMMENT	JOURNAL	FEATURES	SOURCE
Brazil	Unpublished (1995)	Tel: +55-11-2704922 Fax: 55-11-2707001 Email: asimpson@ludwig.org.br	
Laboratory of Cancer Genetics	On May 9, 1995 this sequence version replaced gi:803317.	This sequence was seen in the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethm12.p1?t1=115&t2=115-NTO228-21100-271-h06&t3=2000-11-27&t4=1)	
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, São Paulo-SP,	Seq. primer: PUC 18 forward	Seq. primer: PUC 18 forward	
High quality sequence stop: 290.	Location/Qualifiers	High quality sequence stop: 290.	
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ACCESSION	/note="Organ: nervous tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."	/clone="IMAGE:33011"	
VERSION		/sex="female"	
KEYWORDS		/lab_host="DH10B (ampicillin resistant)"	
REFERENCE		/dev_stag="73 days post natal"	
AUTHORS		/lab_host="Soares infant brain LNIB"	
ORGANISM		/note="Organ: whole brain; Vector: Lambda BA; Site_1: Not I; Site_2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-AATGCGAATTCGGCCGCAAGATTTTTTTTTTT 3'];"	
REFERENCE		/ACTTGGAATTCGGCCGCAAGATTTTTTTTTTT 3'; double-stranded DNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lambda BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Patima Bonaldo."	
AUTHORS			
ORGANISM			
RESULT 8			
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LOCUS	AW973354/C		
DEFINITION	AW973354 MAGE resequences, MAGM Homo sapiens cDNA, mRNA sequence.		
ACCESSION	EST385497		
VERSION	AW973354		
KEYWORDS	AW973354.1 GI:8164576		
REFERENCE			
AUTHORS			
ORGANISM			
RESULT 8			
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LOCUS	AW973354		
DEFINITION	602 bp mRNA linear EST 02-JUN-2000		
ACCESSION	EST385497		
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Query Match	3.4%; Score 60; DB 10; Length 602;	/note="Vector: pBluescriptSKm"
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Oy	1351 ATCCGACGACTTGGAGGCTGAGGTGGTGTACCTGAGTCGGAGTTGAGACCA 1410	1 (bases 1 to 446)
Db	253 ATCCCCACAGTTGGAGGCTGAGGTGGTGTACCTGAGGTCAAGGTCAGAGTCAGACCA 194	Pouatka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R., Mewes,H.W., Weil,B., Amd,C., Osanger,A., Fobo,G., Han,M. and Wienmann,S.
RESULT 9		TITLE EST (Pouatka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R., et al.)
AA558426/C	AA558426	JOURNAL Unpublished (2003)
LOCUS	nk8cc09_s1 NCI CGAP GC2 Homo sapiens cDNA clone IMAGE:101-1792 3,	COMMENT Contact: MIPS
DEFINITION	nk8cc09_s1 NCI CGAP GC2 Homo sapiens cDNA clone IMAGE:101-1792 3, similar to contains_Alu repetitive element;, mRNA sequence.	FEATURES source
ACCESSION	AA558426	ORGANISM Homo sapiens (human)
VERSION	AA558426.1	
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
JOURNAL	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 229)	
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/niccgap.	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
COMMENT	Unpublished (1997)	
REFERENCE	Contact: Robert Strausberg, Ph.D.	
AUTHORS	Email: cgaps_r@mail.nih.gov	
FEATURES source	Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.	
FEATURES source	CDNA Library Preparation: Stratagene, Inc., David B. Krieman, Ph.D.	
FEATURES source	CDNA Library Arraying: Greg Lennon, Ph.D.	
FEATURES source	DNA Sequencing by: Washington University Genome Sequencing Center	
FEATURES source	Clone distribution: NCI-CGAP clone distribution information can be found through the T. M. A. G. E. Consortium at: www-bio.llnl.gov/bcrp/image/image.html	
FEATURES source	Seq primer: -40ml3 fwd. ET from Amersham	
FEATURES source	High quality sequence s/p: 218.	
FEATURES source	Location/Qualifiers	
FEATURES source	1. .229	
FEATURES source	/organism="Homo sapiens"	
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FEATURES source	/db_xref="taxon:9606"	
FEATURES source	/clone="IMAGG_101-1792"	
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FEATURES source	/lab_host="SOLR (kanamycin resistant)"	
FEATURES source	/clone_id="NCI CGAP GC2"	
FEATURES source	/note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XbaI; Cloned unidirectionally. Primer: oligo dt. Bulk germ cell tumor. 5' adaptor sequence: 5' GAATTCGACGAG 3', 3' adaptor sequence: 5' CTCGAGTTTTTTTTT 3'	
FEATURES source	Average insert size: 1.2 kb."	
ORIGIN		
Query Match	3.4%; Score 59; DB 9; Length 229;	
Best Local Similarity	100.0%; Pred. No. 0.018; Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Matches		
Oy	1345 CTGTAATCCCAGCAGTTGGAGGCTGAGGTGGTGTACCTGAGTCAGGAGTC 1403	1 (bases 1 to 68) (synonym: hlcc3)
Db	294 CTGTAATCCCAGCAGTTGGAGGCTGAGGTGGTGTACCTGAGTCAGGAGTC 236	/note="Vector: pTripleX2; Site_1: SfiA; Site_2: SfiB; CDNA-collection"
RESULT 11		
BB061278	BB061278	
LOCUS	IL0-BT0168-031199-135-a05 BR0168 Homo sapiens cDNA, mRNA sequence.	
DEFINITION		
ACCESSION	BB061278	
VERSION	BB061278.1	
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 637)	
AUTHORS	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordim,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.	
JOURNAL	Sequence tags shotgun sequencing of the human transcriptome with ORF expressed sequence tags	
MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	
RESULT 10		
BX506188/C	BX506188	
ILOCUS	446 bp mRNA linear EST 04-SEP-2003	

COMMENT	
Pubmed 10737800 Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br	
FEATURES	source
	/organism="Homo sapiens" <db_xref="taxon:9606" <de>stage="Adult" <clone_id="B70168"
ORIGIN	<p>Query Match 3.3%; score 57; DB 10; Length 637; Best Local Similarity 100.0%; Pred. No. 0.018; Mismatches 0; Indels 0; Gaps 0; Matches 57; Conservative 0; MisMatches 0; Indels 0; Gaps 0;</p> <p>Oy 1340 TCATGCCGTAACTCCACAGCTTGGGAGGCTGAGGTGGTGGATCACCTGAGTC 1396 Db 376 TCATGCCGTAACTCCACAGCTTGGGAGGCTGAGGTGGTGGATCACCTGAGTC 432</p>
RESULT 12	<p>Organism Homo sapiens (human)</p> <p>Locus CD644362/c Definition CD644362 779 bp mRNA linear EST 11-JUN-2003 AgenCourT_14553420 NIA Human H1 Embryonic Stem Cell cDNA Library (Long) Homo sapiens cDNA clone IMAGE:30424873 5', mRNA sequence.</p> <p>Accession CD644362 Version CD644362.1 GI:31816168 EST.</p>
KEYWORDS	
SOURCE	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 779) NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE	Unpublished (1999)
JOURNAL	Contact: Daniela S. Gerhard, Ph.D.
COMMENT	Office of Cancer Genomics National Cancer Institute / NIH Blog: 31 Rm1047 Bethesda, MD 20892 Email: cgabba-r@mail.nih.gov Tissue Procurement: Irene Gnis and Mahendra Rao, NIA cDNA Library Preparation: Yulan Piao and Minoru Ko cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIIL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC C Clone distribution: MGC C Tissue distribution information can be found through the I.M.A.G.E. Consortium/LIIL at: http://image.llnl.gov Plate: NDAM508 row: d column: 02 High quality sequence stop: 650. Location/Qualifiers 1. . 637
FEATURES	source
	/organism="Homo sapiens" <db_xref="taxon:9606" <de>stage="Adult" <clone_id="B70168"
ORIGIN	<p>Query Match 3.3%; score 57; DB 14; Length 779; Best Local Similarity 100.0%; Pred. No. 0.015; Mismatches 0; Indels 0; Gaps 0; Matches 57; Conservative 0; MisMatches 0; Indels 0; Gaps 0;</p> <p>Oy 1340 TCATGCCGTAACTCCACAGCTTGGGAGGCTGAGGTGGTGGATCACCTGAGTC 1396 Db 356 TCATGCCGTAACTCCACAGCTTGGGAGGCTGAGGTGGTGGATCACCTGAGTC 300</p>
RESULT 13	<p>Organism Homo sapiens (cow)</p> <p>Locus CB448183 Definition CB448183 637 bp mRNA linear EST 26-MAR-2003 AgenCourT_70234 MARC 6E0V Bos taurus cDNA 5', mRNA sequence.</p> <p>Accession CB448183 Version CB448183.1 GI:29254565 EST.</p>
KEYWORDS	
SOURCE	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cotariodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovine; Bos.
REFERENCE	1 (bases 1 to 637)
AUTHORS	Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-Mckown, C.G., Wray, J.E. and Keele, J.W.
TITLE	A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL	Unpublished (2003) Contract: Smith TPL USA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390
FEATURES	source
	/organism="Homo sapiens" <db_xref="taxon:9606" <de>stage="Adult" <clone_id="B70168"
ORIGIN	<p>Query Match 3.3%; score 57; DB 14; Length 779; Best Local Similarity 100.0%; Pred. No. 0.015; Mismatches 0; Indels 0; Gaps 0; Matches 57; Conservative 0; MisMatches 0; Indels 0; Gaps 0;</p> <p>Oy 1340 TCATGCCGTAACTCCACAGCTTGGGAGGCTGAGGTGGTGGATCACCTGAGTC 1396 Db 356 TCATGCCGTAACTCCACAGCTTGGGAGGCTGAGGTGGTGGATCACCTGAGTC 300</p>
RESULT 14	<p>Organism Bos taurus (cow)</p> <p>Locus CB448183 Definition CB448183 637 bp mRNA linear EST 26-MAR-2003 AgenCourT_70234 MARC 6E0V Bos taurus cDNA 5', mRNA sequence.</p> <p>Accession CB448183 Version CB448183.1 GI:29254565 EST.</p>
KEYWORDS	
SOURCE	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cotariodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovine; Bos.
REFERENCE	1 (bases 1 to 637)
AUTHORS	Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-Mckown, C.G., Wray, J.E. and Keele, J.W.
TITLE	A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL	Unpublished (2003) Contract: Smith TPL USA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0_990329.

Plate: FQ807 row: L column: 17

Seq primer: GGTATACCACTACATGGG.

FEATURES

source

Location/Qualifiers

1. .637

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/tissue_type="pooled"

/lab_host="DHL0B"

/clone_lib="MARC 6BOV"

/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;

Library made with RNA pooled from multiple tissues

including liver, lung, hypothalamus, pituitary, and

placenta/endometrium."

ORIGIN

Query Match

Best Local Similarity 3.2%; Score 56; DB 11; Length 1287;

Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Accession 1516

LOCUS c16sd10.z1

DEFINITION Hembase: Erythroid Precursor Cells (LCB:cl library) Homo

ACCESSION BU660876

VERSION 1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS 1 (bases 1 to 208)

TITLE Gubin, A.N., Lee, Y.T., Bouffard, G.G. and Miller, J.L.

JOURNAL Gene Expression in Human Erythroid Precursor Cells

COMMENT Unpublished (2002)
Contact: Jeffery L. Miller
Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda, MD

20892, USA
Tel: 301 402 2373

Fax: 301 435 5148

Email: jml@nih.gov

The cl library was constructed by Alexander Gubin, Ph.D. in the

Laboratory of Chemical Biology, NIDDK, NIH. DNA Sequencing and/or

analyses by National Institutes of Health Intramural Sequencing

Center (NISC). More information available at:

<http://hembase.niddk.nih.gov>

Plate: 65 row: d column: 10

Seq primer: 5' lambda-Triplex? Sequencing Primer.

Location/Qualifiers

1. .208

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="c16sd10"

/sex="unknown"

/tissue_type="blood"

/cell_type="Erythroid Precursor Cells"

/mononuclear Cells"

/dev_stage="Precursor erythroblasts; GPA++"

/lab_host=DHSalpha"

/library="Hembase; Erythroid Precursor Cells (LCB:cl

/note="Orjan: blood; Vector: pTriplex2; Site 1: Sfi I;

Site 2: Sfi I; A complementary DNA (cDNA) library from

human erythroid precursor cells was constructed using

SMART PCR (polymerase chain reaction) cDNA library

construction kit (Clontech, Palo Alto, CA) according to

the manufacturer's directions, but with slight

modifications. Briefly, reverse transcription was

performed in the presence of 1 μmol/L peptide nucleic acid

(PNA) oligos

(N-terminal)-biotin-CGC-CAC-CCC-AAG-CTT-G-(C-terminal) and

(N-terminal)-biotin-CTT-CYT-GAA-GTT-CTC-AGG-A-(C-terminal)

. Synthesized cDNA was digested with Sfi I and

size-selected on a 1% agarose gel (>800bp). Large scale

sequencing of the library was performed by the NIH

Intramural Sequencing Center (NISC);

ORIGIN

Query Match 3.2%; Score 55; DB 13; Length 208;
Best Local Similarity 100.0%; Prd. No. 0.12; Mismatches 0; Indels 0; Gaps 0;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1527 CTGCAACCTGGAGGCAGGTGTCAGTCAGCCAGATCGTGCATTGACTCCA 1581
Db 128 CTGACCTGGAGGCAGGTTGAGTCAGTGAGCCGAGATCGTGCATTGACTCCA 182

Search completed: October 1, 2004, 03:51:44
Job time : 4109.41 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model.

Run on: September 30, 2004, 21:45:48 ; Search time 123,742 Seconds
(without alignments)
696.194 Million cell updates/sec

Title: US-10-077-698-5
Perfect score: 1
Sequence: ttggcaagtcaggtaagc.....aaaaaaaaaaaaaaa 1560

Scoring table: OLIGO NUC , Gapox 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*

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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PCUTS_COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1560	100.0	1560	4 US-09-261-599B-5
2	1560	100.0	1560	4 US-09-456-455A-5
3	181	11.6	181	4 US-09-456-455A-14
4	138	8.8	138	4 US-09-455-455A-15
5	44	2.8	1743	4 US-09-261-599B-2
6	44	2.8	1743	4 US-09-456-455A-2
7	38	2.4	241	3 US-09-328-11-472
8	26	1.7	753	3 US-09-232-19-14
9	26	1.7	753	3 US-09-233-20-14
10	26	1.7	753	4 US-09-232-19-14
11	26	1.7	753	4 US-09-232-21-14
12	26	1.7	753	4 US-09-233-19-14
13	26	1.7	1560	4 US-09-261-599B-5
14	26	1.7	1560	4 US-09-456-455A-5
15	26	1.7	16442	3 US-08-781-891-208
16	26	1.7	16442	4 US-09-618-208
17	25	1.6	624	3 US-09-385-924-1
18	25	1.6	694	4 US-09-145-545-23
19	25	1.6	950	3 US-09-241-335-57
20	25	1.6	994	4 US-09-366-887-15
21	25	1.6	1174	4 US-0-16-595-49
22	25	1.6	1243	4 US-09-731-924-1
23	25	1.6	1244	4 US-08-916-442-1
24	25	1.6	1244	4 US-09-317-641-1
25	25	1.6	1513	4 US-09-716-129-23
26	25	1.6	1545	4 US-09-552-023-1
27	25	1.6	1594	4 US-09-016-434-1059

ALIGNMENTS

RESULT 1
US-09-261-599B-5

; Sequence 5, Application US/09261599B
; Patent No. 6395877

; GENERAL INFORMATION:

; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: 14273 Receptor, A NO. 6395877el G-Protein Coupled Receptor
; FILE REFERENCE: 5800-4B, 038800177086
; CURRENT APPLICATION NUMBER: US/09/261-599B
; CURRENT FILING DATE: 1999-02-26
; PRIORITY NUMBER: 09/107,761
; PRIORITY FILING DATE: 1998-06-30
; PRIORITY APPLICATION NUMBER: 09/223,538
; PRIORITY FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Murine ortholog

Query Match Best Local Similarity 100.0%; Score 1560; DB 4; Length 1560;
Matches 1560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCAACTCTAGCGTAGGCCTTCCATGCACTCAGCAGAGGGTTCATGGAGGCC 60
Dy 1 TTGCAACTCTAGCGTAGGCCTTCCATGCACTCAGCAGAGGGTTCATGGAGGC 60

QY 61 TTGACACCATCTGACAGCCACTCAGACTTGTCGGCTTACCGAACATTGAGCGAG 120
Dy 61 TTGACACCATCTGACAGCCACTCAGACTTGTCGGCTTACCGAACATTGAGCGAG 120

QY 121 TCGATGACCTCTGACAGCCAGGCGCGAGCTGCGCACTTCCGGAGCGCTGG 180
Dy 121 TCGATGACCTCTGACAGCCAGGCGCGAGCTGCGCACTTCCGGAGCGCTGG 180

QY 181 GCGGGGCCCGCCGCGCCATGTCAGCTGAGCTGAGCTGAGCTGAGCTGAGCGGCC 240
Dy 181 GCGGGGCCCGCCGCGCCATGTCAGCTGAGCTGAGCTGAGCTGAGCTGAGCGGCC 240

QY 241 CCTGTGACCTCACTGACGCCACTTCCCTTCTCGATGTCAGCGGCCGAC 300
Dy 241 CCTGTGACCTCACTGACGCCACTTCCCTTCTCGATGTCAGCGGCCGAC 300

QY 241 CCCGGGACCAAGTCATGCACTGACGCCACTTCCCTTCTCGATGTCAGCGGCC 300
Dy 241 CCCGGGACCAAGTCATGCACTGACGCCACTTCCCTTCTCGATGTCAGCGGCC 300

QY 301 GGTGTTGTTGAGGCTCTGGAGACCAACCGCTTGGGACTCATCTTGTGCTCACTGC 360
Dy 301 GGTGTTGTTGAGGCTCTGGAGACCAACCGCTTGGGACTCATCTTGTGCTCACTGC 360

Db 541 ACCTGATGACAATGAGCGCAGSGTCACATGGCGCGGTCAACTGGCGCGGTCAACTGGAGC 600
 Qy 601 GCTGGTGTGCTGTGGCTTCGGGGCTTGAGGGCCGGGACTCAGG 660
 Db 601 GCTGGTGTGCTGTGGCTTCGGGGCTTGAGGGCCGGGACTCAGG 660
 Qy 661 CGGCACTCTGGCTTATGGGTACTCGGGCTGGCCCTACATCT 720
 Db 661 CGGCACTCTGGCTTATGGGTACTCGGGCTGGCCCTACATCT 720
 Qy 721 TGTTCGGCGGCGGCTGGCTGGGACTCTGGGTACTCGGGCTGGCCCTACATCT 780
 Db 721 TGTTCGGCGGCGGCTGGCTGGGACTCTGGGTACTCGGGCTGGCCCTACATCT 780
 Qy 781 TGGATTGGCCAACCGCATAGGAGAAATCGGAAATTCGATTTGACAT 840
 Db 781 TGGATTGGCCAACCGCATAGGAGAAATTCGATTTGACAT 840
 Qy 841 TCCCTGGTGGCGGACTGTGTCATGTGATCAGTAATTCAGATCACGAAG 900
 Db 841 TCTTGGTGGCGGACTGTGTCATGTGATCAGTAATTCAGATCACGAAG 900
 Qy 901 CATGGCGSAGAGGCTGGCTGGAGCTGGAGCTGGAGATCTGGAGGT 960
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 Qy 961 CCCAACAGACTACCGACTCTGGACCTCTCTCTCATGTGTCATCA 1020
 Db 961 CCCAACAGACTACCGACTCTGGACCTCTCTCTCATGTGTCATCA 1020
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 Db 1021 TGTGGAGTCCCACATCACCACTCCCTCTCATGTGTCATCA 1080
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 Qy 1381 ACAGCAGGCATCTGGAGGCCGAATTAGGAATTCAGTGTGTCAGTAATATT 1440
 Db 1381 ACAGCAGGCATCTGGAGGCCGAATTAGGAATTCAGTGTGTCAGTAATATT 1440
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 Db 1441 TCTTAAAGAGACTTCATGGGTCTTGTGAACTTTAAGTGTGTGTAT 1500
 RESULT 3
 US-09-456-455A-14
 Sequence 14, Application US/09456455A
 ; Sequence 14, Application US/09456455A
 ; Patent No. 6448005
 ; GENERAL INFORMATION:
 ; APPLICANT: Gluckmann, Maria A.
 ; TITLE OF INVENTION: Receptor, A No. 6448005el G-Protein Coupled Receptor
 ; FILE REFERENCE: MNI-204CP3
 ; CURRENT APPLICATION NUMBER: US/09/456 455A
 ; CURRENT FILING DATE: 1999-2-08
 ; PRIOR APPLICATION NUMBER: 09/107, 761
 ; PRIOR FILING DATE: 1998-06-30
 ; PRIOR APPLICATION NUMBER: 09/223, 538
 ; PRIOR FILING DATE: 1998-12-30
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 15
 ; LENGTH: 138
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-09-456-455A-15
 Query Match 8.8%; Score 138; DB 4; Length 138;
 Best Local Similarity 100.0%; Pred. No. 3-1e-53; Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 969 GACTACCACTCTCCGAGCTCTCTGCTCATGGTGTCCCACCAA 968
 Qy 969 GACTACCACTCTCCGAGCTCTCTGCTCATGGTGTCCCACCAA 968
 Db 61 GACTACCACTCTCCGAGCTCTCTGCTCATGGTGTCCCACCAA 60
 Qy 1 AAGGGCTTACGGCTGAGCTGTCATCTGAGAGCCACGATCCAGTGTGTCACCA 60
 Db ; APPPLICANT: Gluckmann, Maria A.

RESULT 5
 Qy 1029 CCCATCATCATGCCATC 1046
 ; Sequence 2, Application US/09261599B
 Db 121 CCCATCATCATCACCTC 138
 ; GENERAL INFORMATION:
 ; APPLICANT: Glucksmann, Maria A.
 ; TITLE OF INVENTION: 14273 Receptor, A No. 6395877el G-Protein Coupled Receptor
 ; FILE REFERENCE: 5800-AB, 035800177086
 ; CURRENT APPLICATION NUMBER: US/09/261,599B
 ; CURRENT FILING DATE: 1999-02-26
 ; PRIOR APPLICATION NUMBER: 09/107,761
 ; PRIOR FILING DATE: 1998-06-30
 ; PRIOR APPLICATION NUMBER: 09/223,538
 ; PRIOR FILING DATE: 1998-12-30
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 2
 ; LENGTH: 1743
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-261-599B-2

Query Match 2.8%; Score 44; DB 4; Length 1743;
 Best Local Similarity 100.0%; Pred. No. 1.6e-10; Mismatches 0; Indels 0; Gaps 0;
 Matches 44; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 852 GACTGGTCATGTGATCAGTACTCCAAATTACAGATCAC 895
 Db 701 GACTGGTCATGTGATCAGTACTCCAAATTACAGATCAC 744

RESULT 6
 US-09-456-455A-2
 ; Sequence 2, Application US/09456455A
 ; Patent No. 6448005
 ; GENERAL INFORMATION:
 ; APPLICANT: Glucksmann, Maria A.
 ; APPLICANT: Tsai, Fong-Ying
 ; TITLE OF INVENTION: 14273 Receptor, A No. 6448005el G-Protein Coupled Receptor
 ; FILE REFERENCE: MNI-204C93
 ; CURRENT APPLICATION NUMBER: US/09/456,455A
 ; CURRENT FILING DATE: 1998-12-07
 ; PRIOR APPLICATION NUMBER: 09/107,761
 ; PRIOR FILING DATE: 1998-06-30
 ; PRIOR APPLICATION NUMBER: 09/223,538
 ; PRIOR FILING DATE: 1998-12-30
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 2
 ; LENGTH: 1743
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-328-111-472

Query Match 2.8%; Score 44; DB 4; Length 1743;
 Best Local Similarity 100.0%; Pred. No. 1.6e-10; Mismatches 0; Indels 0; Gaps 0;
 Matches 44; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 852 GACTGGTCATGTGATCAGTACTCCAAATTACAGATCAC 895
 Db 701 GACTGGTCATGTGATCAGTACTCCAAATTACAGATCAC 744

RESULT 8
 US-09-232-191-14
 ; Sequence 14, Application US/09232191
 ; Patent No. 6284487
 ; GENERAL INFORMATION:
 ; APPLICANT: Stahl, Andreas
 ; APPLICANT: Hirsch, David J.
 ; APPLICANT: Lodish, Harvey F.
 ; TITLE OF INVENTION: Fatty Acid Transport Proteins
 ; FILE REFERENCE: WII97-21P3ME
 ; CURRENT APPLICATION NUMBER: US/09/232,191
 ; CURRENT FILING DATE: 1999-01-14
 ; EARLIER APPLICATION NUMBER: 60/071,374
 ; EARLIER FILING DATE: 1998-01-15
 ; EARLIER APPLICATION NUMBER: 60/093,491
 ; EARLIER FILING DATE: 1998-07-20
 ; EARLIER APPLICATION NUMBER: 60/110,941
 ; EARLIER FILING DATE: 1998-11-04
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 14
 ; LENGTH: 753
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-232-191-14

Query Match 2.8%; Score 44; DB 4; Length 1743;
 Best Local Similarity 100.0%; Pred. No. 1.6e-10; Mismatches 0; Indels 0; Gaps 0;
 Matches 44; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 852 GACTGGTCATGTGATCAGTACTCCAAATTACAGATCAC 895
 Db 701 GACTGGTCATGTGATCAGTACTCCAAATTACAGATCAC 744

RESULT 7
 US-09-328-111-472
 ; Sequence 472, Application US/09328111
 ; Patent No. 6263333
 ; GENERAL INFORMATION:

RESULT 9
 US-09-232-200-14

; Sequence 14, Application US/09232200A
; Patient No. 6289213
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirach, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WH197-21P3MB
; CURRENT APPLICATION NUMBER: US/09/232,200A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 753
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-232-200-14

Query Match 1.7%; Score 26; DB 3; Length 753;
Best Local Similarity 100.0%; Pred. No. 0.025; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1535 CCTACACAAACAAACAAACAAACAA 1560
Db 726 CCTACACAAACAAACAAACAAACAA 751

RESULT 10

US-09-232-197-14
; Sequence 14, Application US/09232197A
; Patent No. 6310096
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirach, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WH197-21P3MA
; CURRENT APPLICATION NUMBER: US/09/232,197A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 753
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-232-201-14

Query Match 1.7%; Score 26; DB 3; Length 753;
Best Local Similarity 100.0%; Pred. No. 0.025; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1535 CCTACACAAACAAACAAACAAACAA 1560
Db 726 CCTACACAAACAAACAAACAAACAA 751

RESULT 12

US-09-232-195-14
; Sequence 14, Application US/09232195A
; Patent No. 6657049
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirach, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WH197-21P3MD
; CURRENT APPLICATION NUMBER: US/09/232,195A
; CURRENT FILING DATE: 1999-01-04
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 753
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-232-195-14

Query Match 1.7%; Score 26; DB 4; Length 753;
Best Local Similarity 100.0%; Pred. No. 0.025; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1535 CCTACACAAACAAACAAACAAACAA 1560
Db 726 CCTACACAAACAAACAAACAAACAA 751

RESULT 11

RESULT 13
US-09-261-599B-5/c
Sequence 5, Application US/09261599B
; Patent No. 639877
GENERAL INFORMATION:
APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: 14273 Receptor, A No. 6395877e1 G-Protein Coupled Receptor
FILE REFERENCE: 5900-4B 035800177086
CURRENT APPLICATION NUMBER: US/09/261,599B
CURRENT FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 09/107,761
PRIOR FILING DATE: 1998-06-30
PRIORITY APPLICATION NUMBER: 09/223,538
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 1560
TYPE: DNA
ORGANISM: Murine ortholog
US-09-261-599B-5

Query Match 1.7%; Score 26; DB 4; Length 1560;
Best Local Similarity 100.0%; Pred. No. 0.025; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGCCAAAGCTCAGCTAACGCTTCTTCC 27
Db 932 TGCCAAAGCTCAGCTAACGCTTCTTCC 907

RESULT 14
US-09-456-455A-5/c
Sequence 5, Application US/09456455A
; Patent No. 6448005
GENERAL INFORMATION:
APPLICANT: Glucksmann, Maria A.
APPLICANT: Tsai, Fong-Ying
TITLE OF INVENTION: 14273 Receptor, A No. 6448005e1 G-Protein Coupled Receptor
FILE REFERENCE: MNJ-204C03
CURRENT APPLICATION NUMBER: US/09/456,455A
CURRENT FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: 09/107,761
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: 09/223,538
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 1560
TYPE: DNA
ORGANISM: Murine ortholog
US-09-456-455A-5

Query Match 1.7%; Score 26; DB 4; Length 1560;
Best Local Similarity 100.0%; Pred. No. 0.025; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGCCAAAGCTCAGCTAACGCTTCTTCC 27
Db 932 TGCCAAAGCTCAGCTAACGCTTCTTCC 907

RESULT 15
US-08-791-891-208
; Sequence 208, Application US/08781891
; Patent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.

Query Match 1.7%; Score 25; DB 3; Length 16442;
Best Local Similarity 100.0%; Pred. No. 0.023; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1535 CCTCAAAAAAACAAAAAA 1560
Db 11978 CCTCAAAAAAACAAAAAA 12003

Search completed: October 1, 2004, 03:56:18
Job time : 126.742 secs

GenCore version 5.1.6
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Om nucleic - nucleic search, using sw model

Run on: September 30, 2004, 19:57:17 ; Search time 3672.59 Seconds
 (without alignments)
 12684.514 Million cell updates/sec

Title: US-10-077-698-5

Perfect score: 1560

Sequence: 1 ttgccaagtcacggtaagg.....aaaaaaaaaaaaaaaaaa 1560

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 27513289 Seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : EST:*

1: em_estba:*

2: em_estbhum:*

3: em_estbin:*

4: em_estmu:*

5: em_estcov:*

6: em_estapl:*

7: em_estcc:*

8: em_htcc:*

9: gb_est1:*

10: gb_est2:*

11: gb_hcc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pbn:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT	1	AV021454	AV021454	AV021454	692 bp mRNA linear EST 23-OCT-2001
LOCUS					DEFINITION Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA
DEFINITION					clone 119023B03, mRNA sequence.
ACCESSION					AV021454
VERSION					AV021454.2 GI:16356377
KEYWORDS					EST, SOURCE, ORGANISM
SOURCE					Mus musculus (house mouse)
ORGANISM					Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE					1 (bases 1 to 692)
AUTHORS					Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hayashizaki,Y., Hara,A., Hiramoto,K., Hori,F., Ishii,I., Ito,M., Kawai,J., Kondo,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shikai,T., Sogane,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takenaka,Y., Tanaka,T., Tovar,J., Muramatsu,M., and Hayashizaki,Y.
TITLE					RIKEN Mouse ESTB (Arakawa,T., et al. 2001)
JOURNAL					Unpublished (2001)
COMMENT					On May 11, 1999 this sequence version replaced g1:4798446.
CONTACT					Contact: Chie Owa
GENOME					Science Laboratory
RIKEN					3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel:	81-298-36-9145	Db	449		508
Fax:	81-298-36-9098	OY	1262	GTCGTGTTTCCAGCAACTAGCTCTGGCAGGTGACCCGGTGTGATGAAAG	1321
Email:	genome-res@rci.riken.go.jp	Db	509	GTCTGTTTTCAGCTACTACCTCTGGTGCAGTGAAAG	568
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)	OY	1322 GGACTTACTCAGGAAGGCCAACAGTGCGCCCTGCTTAAATCCGACTTCGA	1381	
wagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsurra, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)	Db	569 GGACTTACTCAGGAAGGCCAACAGTGCGCCCTGCTTAAATCCGACTTCGA	628	
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y., and Hayashizaki, Y.	Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)	OY	1382 CACAGGATCTGGACCCAGAAATTAGGATGATGCGTCAGTAAATAATT	1441	
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.	Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)	Db	629 CAGCAGGATCTAGGACCCAGAAATTAGGATGATGCGTCAGTAAATAATT	688	
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.	preparation of cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissue.	OY	1442 CC 1443		
FEATURES source	Location/Qualifiers	Db	689 CC 690		
1. -592	/organism="Mus musculus"	RESULT	2		
/mol_type="mRNA"	/strain="C57BL/6J"	AV025152	AV025152		
/db_xref="Taxon:10090"	/clone="1190023B03"	DEFINITION	AV025152 Mus musculus adult C57BL/6J lung	Mus musculus mRNA sequence.	
/sex="mixed"	/dev_stage="18-day embryo"	ACCESSION	1200010P15, mRN		
/clone_lib="Mus musculus 18-day embryo C57BL/6J"	/clone	VERSION	AV025152		
ORIGIN		KEYWORDS	AV025152.2	EST	
Query Match	38.6%; Score 602; DB 9; Length 692;	SOURCE	GI:15431435		
Best Local Similarity	100.0%; P-ped. No. 0;	ORGANISM	Mus musculus		
Matches 602; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 721)		
OY	842 CTCTGTGCGGGAGCTGGCATGTGTGATGAGTACTCCAAATTACAGATCAGAAGC 901	AUTHORS	Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Kono, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Togawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Tova, T., Muramatsu, M. and Hayashizaki, Y.		
Db	89 CTCTGTGCGGGAGCTGGCATGTGTGATGAGTACTCCAAATTACAGATCAGAAGC 148	TITLE	RIKEN Mouse ESTs (Arakawa, T., et al. 2001)		
OY	902 ATCCGGAGAGGGCTAACCTGAGCTTGCCATACTCTGAGAGCCACAGATGGAGTC 961	JOURNAL	Unpublished (2001)		
Db	149 ATCCGGAGAGGGCTAACCTGAGCTTGCCATACTCTGAGAGCCACAGATGGAGTC 208	COMMENT	On May 11, 1999 this sequence version replaced gi:4802144.		
OY	962 CTCAGAACAGTACCGACTCTTCCGACGCTCTCCCTGCTCATGTTCTCTCAT 1021	CONTACT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222		
Db	209 CCAACAGACTACCGACTCTTCCGACGCTCTCCCTGCTCATGTTCTCTCAT 268	EMAIL	Email: genome-res@gsc.riken.go.jp/ URL:http://genome.gsc.riken.go.jp/		
OY	1022 GTGGAGTCCATCATCATCACATCCTCTCTGAGCTGAGCTGAGCTGAGCT 1081	PREPARED BY	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)		
Db	269 GTGGAGTCCATCATCATCACATCCTCTGAGCTGAGCTGAGCTGAGCT 328	WAGI	wagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsurra, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
OY	1082 GTCTCATCTGGCATCCCTTCTCTGAGCTGAGCTGAGCTGAGCT 1141	REVIEWED BY	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)		
Db	329 GGTCTCATCTGGCATCCCTTCTCTGAGCTGAGCTGAGCTGAGCT 388	REVISED BY	Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y., and Hayashizaki, Y.		
OY	1142 AAACCCATACATGTCACACATGTCGCTGTCAGAACGATGGAGATTTGCTG 1201	COMPUTER	Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)		
Db	389 AACCCCATACATGTCACACATGTCGCTGTCAGAACGATGGAGATTTGCTG 448	STRUCTURE	Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T., Isaki, Y., and Hayashizaki, Y.		
OY	1202 CTCCTTTTCAGAGAAGGGGCCATTITACAGATACGTCCTGTCAGGAAATGACTT 1261	COMMENT	Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.		

RESULT 4

LOCUS	BUS22456	870 bp	mRNA	linear	EST 13-SEP-2002
DEFINITION	AGENCOURT 10153856 NCI_CGAP_Co24	Mus musculus	CDNA clone		
ACCESSION	IMAGE:6528871_5'	mRNA sequence.			
VERSION	BUS22456.1	GI:22829982			
KEYWORDS	EST				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NIH-MGC http://mgc.nci.nih.gov/. Unpublished (1999)				
AUTHORS	I (bases 1 to 870)				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL					
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgsbps-@email.nih.gov Tissue Procurement: The Cepko Laboratory cDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: AgenCourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.lnl.gov Plate: LNLN14128 row: b column: 07 High quality sequence stop: 615.				

FEATURES

source	1. .870	Location/QualifierB	/organism="Mus musculus"	/molType="mRNA"	/strain="FVB/N"	/db_xref="taxon:10090"	/clone="IMAGE:6528871_5'	/lab_host="DNLN0B (T1 phage-resistant)"	/clone_lib="NCI CGAP Co24"	/notes=Organ colon Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."	ORIGIN
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Query Match 30.8%; Score 481; DB 13; Length 870; Best local similarity 99.4%; Prcd. No.; Matches 681; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 711 CTCTACATCTGTTCCGGCTGGTCCCAGGCAAGAAATTCCG 770

Db 532 CTCTGACATCTGTTCGGCGTGTGTCCTCAGCTGGCTTCGGGGAGAACATTCG 591

Qy 771 ATTCGACATTGATTGGCCACCGCTAGAGAAATCTCGGATGTGTTTGAG 830

Db 592 ATTCGACATTGGATGCCAACCGCTAGAGAAATCTCGGATGTGTTTGAG 651

Qy 831 ACTTGACTCTCTGGTGGCGGAATGGCTGATGTCAGTACTCCAAATTAG 890

Db 652 ACTTGACTCTCTGGTGGCGGAATGGCTGATGTCAGTACTCCAAATTAG 711

Qy 891 ATCGAAGAGCATGGCGAGAGGC 950

Db 712 ATCACGAAAGCATCGGGAGAGCTAGCTGAGCTTGACTCTGAGAGC 771

Qy 951 ATCCGAGTG 959

Db 772 ATCCGAGTG 780

RESULT 5

LOCUS	BUS22608	875 bp	mRNA	linear	EST 13-SEP-2002
DEFINITION	AGENCOURT 10154009 NCI_CGAP_Co24	Mus musculus	CDNA clone		
ACCESSION	IMAGE:652120_5'	mRNA sequence.			
VERSION	BUS22608.1	GI:22830134			
KEYWORDS	EST				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NIH-MGC http://mgc.nci.nih.gov/. Unpublished (1999)				
AUTHORS	I (bases 1 to 875)				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL					
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgsbps-@email.nih.gov Tissue Procurement: The Cepko Laboratory cDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: AgenCourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.lnl.gov Plate: LNLN14128 row: 1 column: 16 High quality sequence stop: 653.				

FEATURES

source	1. .875	Location/Qualifiers								
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Db 108 GCGGACCAACGGTGTGTTGAGCTGAGCACACGTCCTGCGGCTCACTTGTG 167

Qy 351 GTCTCACTCTGGCCACAGTGTGCTCTAGCTGTTGGGGAGCCGGGGAGGG 410

Db 168 GTCTCACTGCTGGCAAGCTGTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 227

Qy 411 GCGTCAGGCCAGCCCTGGTGTCAACCTCTCTGGGGGATGCTTACAGGGCATC 470

Db 228 GCGACAGCAGCTGGTGTCAACCTCTCTGGGGAGTTGCTCAGGGCTTC 287

Qy 471 CCTCTAGTGCTCTGCTGCTGCTGACTCTGAGSCACCAAGCTGCTGCTG 347

Db 531 CTCTCTCTACCTGAGACANTGAGGGCACTGCTGAGCTCTCACCTGCTGCTG 590

Db 348 CTGCTCTCTACCTGAGACANTGAGGGCACTGCTGAGCTCTCACCTGCTG 407

Qy 591 AGCTGGGGCATGGTGTGATGTCATGGCTCGGGCTTGGGGGGGGGGGGGG 650

Db 408 AGCTGGAGGAGCTGGTGTGATGTCATGGCTCGGGCTTGGGGGGGGGGGG 467

Qy 651 CGACTCTGGGGGCACTCTCTGCTTCTATGGGTCTCTCGCGCTGCGCTGCC 710

Db 468 CGGACTCTGGGGGCACTCTGCTTCTATGGGTCTCTCGCGCTGCGCTGCC 527

Qy 711 CTCTACATCTGTTGGCGGACTCTCATGGTGTGATGTCAGTACTCCAAATTAG 770

Db 648 ACTTGACTCTCTGGCGGACTCTCATGGTGTGATGTCAGTACTCCAAATTAG 707

Qy 891 ATCGAAGAGCATGGCGAGAGGC 915

Db 708 ATCACGAAAGCATCGGGAGAGGC 732

ORIGIN		KEYWORDS			
SOURCE	EST.	MATERIAL	ORGANISM	DEFINITION	ACCESSION
Query Match	29.8%	Score 465; DB 13; Length 875;	Mus musculus (house mouse)	/organism="Mus musculus"	BQ936343
Best Local Similarity	99.4%	Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;	Mus musculus	/mol-type="mRNA"	BQ936343
Matches	665;	Conservative 0; Mismatches 4; Indels 0; Gaps 0;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; lab host="DH10B" /clone-lab="NCI CGAP_Co24" /note="Organ: colon; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: SAI1; Cloned unidirectionally. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."	/strain="FVB/N"	IMAGE:6488067 5', mRNA Sequence.
Qy	84	CCTCGCACACCTGTGACCGTCACTGCACTCCATTCCTCTCGATGTCAG 143	NIH-MGC http://mgc.ncbi.nlm.nih.gov/	/db-xref="taxon:10020"	B0936343-1 GI:22151726
Db	291	GCGGACCCACGGTTGTTGAGCCTGGAGACCAACCGCTCTGGAACTCTCTGTC 350	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	/clone="IMAGE:6529120"	B0936343
Qy	144	GCGGACCCACGGTTGTTGAGCCTGGAGACCAACCGCTCTGGAACTCTCTGTC 203	Contact: Robert Strausberg, Ph.D.	/dev-stage="P100B"	COMMENT
Db	351	GTCCTACTGCTGGCAACGTGTTGCTAGTGCTGTTGCTAGTGCTGCTGGCTGG 410	Email: cgaps@remail.nih.gov	/db-xref="taxon:10090"	cdna Library Preparation: Life Technologies, Inc.
Qy	204	GTCCTACTGCTGGCAACGTGTTGCTAGTGCTGCTGGCTGGCTGGCTGG 263	DNA Sequencing by: The I.M.A.G.E. Consortium (LML)	/clone="IMAGE:6488067"	DNA
Db	411	GCGTCGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 530	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LML at:	/tissue="tumor, biopsy sample"	Tissue
Qy	264	GCGACACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 323	http://image.lnl.gov	/dev-stage="P5 months"	Unpublished
Db	471	CCTCTAGT 530	Plate: LLM14034 row: b column: 04	/lab-host="DH10B"	Site 1: NotI; Cloned unidirectionally. Primer: Oligo dT.
Qy	324	CCTCTAGT 383	Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH	/clone-lab="NCI CGAP Mam2"	Site 2: SAI1; Cloned unidirectionally. Primer: Oligo dT.
Db	531	CTGCTCTCTCTAGTGTGACATACTGAGGAGGAGCTGTGAGATCTCTACACTGGGGTC 590	CDNA Library Arrayed by: Agencourt Bioscience Corporation	/note="Organ: mammary; Vector: PCMV-SPORT6; Site_1: SAI1; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.	384 CTGCTCTCTAGTGTGACATACTGAGGAGGAGCTGTGAGATCTCTACACTGGGGTC 443
Qy	591	AGCCTGGAGCCATGGTGTGATCGTGGCCCTCCGGGGCTTGAGGGGGCGGG 650	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LML at:	/db-xref="taxon:10090"	384 CTGCTCTCTAGTGTGACATACTGAGGAGGAGCTGTGAGATCTCTACACTGGGGTC 443
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Qy	651	CGGACTCAGGGGGCACTGCTGCTGCTTCAATATGGGTACTCGCGGCTGCGCC 710	Plate: LLM14034 row: b column: 04	/tissue="tumor, biopsy sample"	384 CTGCTCTCTAGTGTGACATACTGAGGAGGAGCTGTGAGATCTCTACACTGGGGTC 443
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Qy	771	ATTGACATGGATGCCAACCGCATAGGAGAATCTCTGCTGGCTGGCTGGCTGGCTGG 830	3. (bases 1 to 928)	/note="Organ: mammary; Vector: PCMV-SPORT6; Site_1: SAI1; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.	384 CTGCTCTCTAGTGTGACATACTGAGGAGGAGCTGTGAGATCTCTACACTGGGGTC 443
Db	624	ATTGACATGGATGCCAACCGCATAGGAGAATCTCTGCTGGCTGGCTGGCTGGCTGG 683	4. (bases 1 to 928)	Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH	384 CTGCTCTCTAGTGTGACATACTGAGGAGGAGCTGTGAGATCTCTACACTGGGGTC 443
Qy	891	ATCACCAA 899	5. (bases 1 to 928)	384 CTGCTCTCTAGTGTGACATACTGAGGAGGAGCTGTGAGATCTCTACACTGGGGTC 443	384 ATCACCAA 752
Db	744	ATCACCAA 752	6. (bases 1 to 928)	384 ATCACCAA 752	
RESULT 6		ORIGIN			
BQ936343	928 bp	mRNA	linear	EST 21-AUG-2002	
LOCUS	10013769	NCI CGAP Mam2	Mus musculus cDNA clone		
DEFINITION					
IMAGE:6488067	5'	mRNA Sequence.			
ACCESSION					
VERSION					

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RESULT	7		Do	122 TGGGTTCTCGCGCTGGCCCTACACTCTGCTTCGGTGTGGTCCCGAG	181
LOCUS	BX527210 BX527210	537 bp mRNA linear EST 27-JUN-2003	QY	741 CGCCTCCGGGGGACAGGAATTCCGATTGCAATTGGCCAAACCGATA	800
DEFINITION	BX527210 Soares_mammary_gland NbMG Mus musculus cDNA clone		Do	182 CGCCTCCGGGGGACAGGAATTCCGATTGCAATTGGCCAAACCGATA	241
ACCESSION	IMA6998K072670 ; IMAGE:1067646, mRNA sequence.		QY	801 GGAGAAATCTCATGGATGTTGAGCTTGACCTCTGGTCCGGGACTCTGTC	860
VERSION	BX527210.1 GI:32304990		Do	242 GGAGAAATCTCATGGATGTTGAGCTTGACCTCTGGTCCGGGACTCTGTC	301
KEYWORDS	EST.		QY	851 ATGGTACAGTACTCCAAATTGAGATCAGGAAATTCCGATTGCAATTGGCCAAACCGATA	920
SOURCE	Mus musculus (house mouse)		Do	302 ATGGTACAGTACTCCAAATTGAGATCAGGAAATTCCGATTGCAATTGGCCAAACCGATA	361
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AUTHORS	Heil.O., Ebert.I., Neubert.P., Peters.M., Radelof.U., Schneider.D. and Korn.B.		QY	981 TTGGCAGCTCTCCCTCATGGTTCTCTCATATGGAGTCAGTGGAGAGCTTCAG	1040
TITLE	Mouse UnigeneSet - RZPD		Do	422 TTGGCAGCTCTCCCTCATGGTTCTCTCATATGGAGTCAGTGGAGAGCTTCAG	481
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COMMENT	Contact: Ina Rolfs		Do	482 ACCATCCCTCATGGTCAAACTTCCGGAGGAGCTGGTCATGGCATT 537	
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SOURCE		BB609925			
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		ACCESSION	BB609925		
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		REFERENCE	1 (bases 1 to 671)		
		AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hayagaki,T., Hara,A., Hiramoto,K., Hori,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.		
		TITLE	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)		
		JOURNAL	Unpublished (2001)		
		COMMENT	Contact: Yoshinide Hayashizaki		
			Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute		
			The Institute of Physical and Chemical Research (RIKEN)		
			1-7-22 Subshiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan		
			Tel: 81-45-503-9222		
			Fax: 81-45-503-9216		
			Email: genome-res@gsc.riken.go.jp/		
			URL: http://genome.gsc.riken.go.jp/		
			Carninci,P., Shiba,T., Hayashizaki,Y., Sugahara,Y., Shiota,K.,		
			Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		
			Normalization and subtraction of cap-trapper-selected cDNAs to		
			prepare full-length cDNA libraries for rapid discovery of new		
			genes. Genome Res. 10 (10) 1617-1630 (2000)		
			Waga,K., Fujisawa,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,		
			Watanuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,		
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Db 196 GATCCGAGCTCCAAACAGACTACCGACTCTTCGCACGCTTCTCTGCTCATGGTTTC 255

further details.
A mouse tissue-

Qy 1010 CTCCTCATGAGCCATCACCCTCTCATTTGATCCAACTT 1062

SOURCE 1: :637

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VERSION BB609814.1 GI:16451529
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
 1 (bases 1 to 637)
 Arakawa,T., Carrinici,P., Fukuda,S., Furuno,M., Hanagaki,T.,
 Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
 Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
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 Sogabe,Y., Suzuki,H., Tagami,M., Shigenaga,A., Takahashi,F.,
 Takeda,T., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
TITLE
 RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
JOURNAL
 Unpublished (2001)
COMMENT
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Research, Riken, Saitama, Japan

bioactive molecule generation research group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute of Science and Technology, 2-17-1 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: +81-45-503-9235 Fax: +81-45-503-9235

✉ Email: 011-5705-2240
Email: genome-rca@gscc.riken.go.jp,
[URL:<http://genome.gscc.riken.go.jp/>](http://genome.gscc.riken.go.jp/)
Carnici, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, T., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trap-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. *Genome Res.* 10 (10), 1617-1630 (2000)
wagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,

Watanuki, M., Yoneda, Y., Isekiwa, T., Ozawa, K., Tanaka, T., Matsubara, S., Kawaji, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)

Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kyosawa, H., Yamamoto, I.,
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and

Hayashizaki, Y. International Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. *Mamm. Genome*. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for

further details.
A mouse tissue.

BF580577	BF580577	647 bp mRNA linear EST 12-DEC-2000	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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REFERENCE	(bases 1 to 647)		
AUTHORS	NIH-MCC http://mgc.nci.nih.gov/		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
CONTACT	Contact: Robert Strausberg, Ph.D. Email: cgabs@remail.nih.gov		
TISSUE	Procurement: Jeffrey B. Green, M.D.		
PROCUREMENT	cDNA Library Preparation: Life Technologies, Inc.		
LIBRARY	CDNA Library Arrayed By: The I.M.A.G.E. Consortium (LNU)		
SEQUENCING	DNA Sequencing by: Incyte Genomics, Inc.		
CLONE	Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LNU at:		
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Db	181 CATGCCCTTCCTGGCTGGSCCTCAGCTT 214		
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REFERENCE	The WashU-HMM Mouse EST Project		
AUTHORS	Unpublished (1996)		
JOURNAL	Contact: Marra M/Mouse EST Project		
COMMENT	Fax: 314 286 1810		
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model
Run on: September 30, 2004, 19:03:02 ; Search time 6615.8 Seconds
(without alignments)
11419.163 Million cell updates/sec
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Perfect score: 1743
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Gapop_60.0 , Gapext_60.0
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Word size : 0
Total number of hits satisfying chosen parameters: 6940544
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Listing first 45 summaries

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2: gb_baa:
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4: gb_in:
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6: gb_pat:
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9: gb_pr:
10: gb_rc:
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8	926	53.1	1086	6 AX498184	AX498184 Sequence
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13	391	22.4	1737	6 AX539396	AX539396 Sequence
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38	67	3.8	15282	9 AL133255	AL133255 Human DNA
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ALIGNMENTS

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							1 (bases 1 to 1743)
							Glucksmann, M.A. and Tsai, F.Y.
							14273 receptor, a G-protein coupled receptor
							Patent: JP 200252201-A 1 23-JUL-2002;

Db	1289	GCTGTGTCACCAAGTTCTAATTTCCTTAAATGGATTGCGCCAGTGCA	1348
Qy	1335	GTCGTCTAGCCTGTAATCCAGCTGTTGGAGCTGAGGATCCTGAT	1394
Db	1349	GTGGTCATGCCTGTAATCCAGCTGTTGGAGCTGAGGATCCTGAT	1408
Db	1409	CAGGAGTCGAGACCAACTGACCAACATGGAGACCCCGTCTACT	1458
Qy	1395	CAGGAGTCGAGACCAACTGACCAACATGGAGACCCCGTCTACT	1444
Db	1438	ATGGTGTGTCATCGACCTGAGGAGCTGACCTGAGGAGCTGACCT	497
Qy	452	ATGGTGTGTCATCGACCTGAGGAGCTGACCTGAGGAGCTGACCT	511
Qy	512	GTGCTGTCGGCGCTCTCTGGGCTATTGGCGCTCTGGCTCTGGCT	571
RESULT 6			
LOCUS	AX168141		
DEFINITION	Sequence 59 from Patent WO0142288.	1321 bp	DNA
ACCESSION	AX168141		
VERSION	AX168141.1		
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
AUTHORS	Burford, N., Baughn, M.R., Au-Young, J., Yang, J., Lu, D.A. and Reddy, R.		
TITLE	G-protein coupled receptors		
JOURNAL	Patent: WO 0142288-A 59 14-JUN-2001; Incyte Genomics, Inc. (US)		
FEATURES			
source	1..1321		
ORIGIN			
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Best Local Similarity	99.8%	Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;	
Matches	1181; Conservative 0;		
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Db	18	CTGGCCGCCGGAATGTCCTCTGATGCGCGCGAACGCGGCCCTGGCAC	77
Qy	92	CTGGGAGCAACGCAACGCAACCGCTTCCTCTCGACGTAAGGGGACCAACGG	151
Db	78	CTGGGAGCAACGCAACGCAACCGCTTCCTCTCGACGTAAGGGGACCAACGG	137
Qy	152	CTGGTCTGGCGCGGTGAGACACCGTGTCACTTGTCAAGTGCTCTG	211
Db	138	CTGGTCTGGCGCGGTGAGACACCGTGTCACTTGTCAAGTGCTCTG	197
Qy	212	GCGAACGTTGCGACCTCTGGTGTGGTGGCGCGGCGACTGCCRC	271
Db	198	GCGAACGTTGCGACCTCTGGTGTGGTGGCGCGGCGACTGCCRC	257
Qy	272	CTGGTCTGGCGCGGTGAGACACCGTGTCACTTGTCAAGTGCTCTG	331
Db	258	CTGGTCTGGCGCGGTGAGACACCGTGTCACTTGTCAAGTGCTCTG	317
Qy	332	GCGGTGGCTGTAATTCCTGCTGCTGCTGCTGCTGCTGCTGCT	391
Db	318	GCGGTGGCTGTAATTCCTGCTGCTGCTGCTGCTGCTGCTGCT	377
Qy	392	GTCATGACCTGAGGCGAGGCGACCACTCTGGCGACCGCTGCTGCT	451
Db	378	GTCATGACCTGAGGCGAGGCGACCACTCTGGCGACCGCTGCTGCT	437
Qy	452	ATGGTGTGTCATCGACCTGAGGAGCTGACCTGAGGAGCTGACCT	511
Db	438	ATGGTGTGTCATCGACCTGAGGAGCTGACCTGAGGAGCTGACCT	497
RESULT 7			
LOCUS	AL356214		
DEFINITION	Human DNA sequence from clone RP1-30E16 on chromosome 10, complete sequence.	163964 bp	DNA
ACCESSION	AL356214		
VERSION	AL356214.20		
KEYWORDS	HTG.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
AUTHORS	Brown, A.		
TITLE	Direct Submission		
JOURNAL	Submitted (13-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: hungry@sanger.ac.uk Clone requests: cloner@east.sanger.ac.uk		
COMMENT	On Apr 14, 2001 this sequence version replaced gi:13160256. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.		

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following given abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL:, Sw:, SWISSPROT:, Tr:, TREMBL:, Wp:, WORMPDB; Information on the WORMPDB database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpdb This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/CGP/Ch10>
RP11-30B16 is from the library RPCI-11-1 constructed by the group of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
VECTOR: pBAC3.6
This sequence is the entire insert of clone RP11-30B16. The true left end of clone RP11-43J02 is at 129920 in this sequence. The true right end of clone RP11-313N18 is at 82571 in this sequence.

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repeat_region 11413. .11528  
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repeat_region 11536. .11719  
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/note="CfG island"
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RESULT 12									
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QY	365	CGCTGCTGGCACCTCTCTCTACCTGATGACCCCTGAGGCGAGGGTACCATC	424	61	CTGGGAAAGTGGCCCTGGCTGGCTGGCCACAGACGGCGACTGCC	120	Db	61	CTGGGAAAGTGGCCCTGGCTGGCTGGCCACAGACGGCGACTGCC
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Db	379	ACGCTGGCCGGCTAGCTGACGGCTGGCTGGCCACAGACGGCGACTGCC	438	329	CTGGCGGG	388	QY	329	CTGGCGGG
QY	485	CGGGCTCTGG	544	181	CTGGCGGG	240	Db	181	CTGGCGGG
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QY	665	GATGCTCTTGTGACTCTGATGTTGGCTGGCCAGGACTGGCTGGCTGGCTGG	724	361	GCAGTGCTGGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	420	Db	361	GCAGTGCTGGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
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QY	725	TCCAATTTCAGA 740		421	TTCTT 425		Db	421	TTCTT 425
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LOCUS	Sequence	87	from Patent WO03000893.						
DEFINITION									
ACCESSION	AX657504	AX657504.1	GI:29160243						
VERSION									
KEYWORDS									
SOURCE									
ORGANISM									
REFERENCE									
AUTHORS	Martinez,R.M. and Sigurdsson,G.T.								
JOURNAL	Nucleic acids encoding G protein-coupled receptors								
FEATURES	Decode Genetics BHF. (IS)								
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	/translation="RKLAVETVLUPIAVSLIGVNLVLRARRRGATACLU								
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ORIGIN									
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Db	61	GAAATTTTTCTGCTTGCTTCCAGAACGGGCCATTACAGAACATGTG								120
Qy	1096	CAAAAGAAATGACTTGCGATTATTCGCTTAATTCTTATAGCGGATTTCAC								1155
Db	121	AAAAGAAATGACTTGCGATTATTCGCTTAATTCTTATAGCGGATTTCAC								180
Qy	1156	ACCTGGGAGCTGGCATGCTTTAACAGAGTCATTCCAGTACCTCCATCAGTG								1215
Db	181	ACCTGGGAGCTGGCATGCTTTAACAGAGTCATTCCAGTACCTCCATCAGTG								240
Qy	1216	ACCTGCTTAAAGAAATGACCTATGCAATAGACATCCACAGCGTGGTAATTAGG								1275
Db	241	ACCTGCTTAAAGAAATGACCTATGCAATAGACATCCACAGCGTGGTAATTAGG								300

Search completed: October 1, 2004, 01:41:55
 Job time : 6621.8 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 19:01:32 ; Search time 635.881 Seconds
 (without alignments) 11644.646 Million cell updates/sec

Title: US-10-077-698-2

Perfect score: 1743

Sequence: tccggactatgttcttagacgg.....aaaaaaaaggcg 1743

Scoring table: OLIGO_NUC
 Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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- 3: geneseqn20008:*
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- 8: geneseqn2003bs:*
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- 10: geneseqn2004ab:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description
1	1743	100.0	1743	Aaa64345 DNA encoded
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3	1328	76.2	1458	AA166039 Human G_P
4	1109	63.5	1109	Abx10527 DNA encoded
5	1086	62.3	1086	AB573343 cDNA enco
6	1081	62.0	1321	AD008854 Human G_P
7	1035	59.4	1086	Abs73398 DNA encoded
8	1035	59.4	1086	AC60998 cDNA enco
9	1035	59.4	1086	Adb47641 Human cDN
10	984	1086	8	Ab573399 DNA encoded
11	926	53.1	1086	AB504869 Human G_P
12	913	52.4	1742	AA249745 Human 142
13	746	42.8	745	Ab21432 Human gene
14	586	33.6	632	AC61000 Novel human
15	586	33.6	632	ADb7644 Human cDN
16	559	32.1	1065	ADC07012 Human GPC
17	550	31.6	3173	Ab504869 Human G_P
18	425	24.4	933	AD12755 Human GPC
19	391	22.4	1737	Ab242599 Human G_P
20	337	19.3	388	AB08489 Human GPC
21	326	18.7	1104	AA542815 Human G_P
22	300	17.2	2	AA213607 Human gene
23	298	17.1	760	Aax99045 Human gene

CC to screen for agonist and antagonists. The antibodies are used for diagnostic applications, and to assess abnormal tissue distributions or abnormal expression during development. The antibodies are also useful for tissue typing, and in forensic identification, as well as for inhibiting receptor function. The 14273 polymucleotides can be used to detect genetic alterations in the 14273 gene, and as a source of primers and probes. The 14273 polymucleotides and polypeptides are also useful as a target for diagnosis and treatment of receptor-mediated disorders, especially cardiovascular diseases such as congestive heart failure caused by cardiac myocyte hypertrophy

XX Sequence 1743 BP; 380 A; 479 C; 451 G; 433 T; 0 U; 0 Other;

Query Match Best Local Similarity 100.0%; Score 1743; Length 1743; Matches 1743; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	1 TCCGACTAGTCTAGACGCCGGGGCCACGGCGGGGAATGTCCCTGATGCC	60	Db	901 CTCCTCTCATGGCTCTCTCTCATATGTTGGAGCCCATCATCACCCTCT	900
QY	61 GCGGGCAGGGGGCACGCCGGGGCTGGGAGCAGCGCCAGGGGAATGTCC	120	Db	960 CATCTGATCCAGACTCAAGCAGACCTGGGCTGGGGCTCTCTCTCTGGGT	960
Db	61 GCGGGCAGGGGGCACGCCGGGGCTGGGAGCAGCGCCAGGGGAATGTCC	120	Db	960 CATCTGATCCAGACTCAAGCAGACCTGGGCTGGGGCTCTCTCTCTGGGT	960
QY	121 CTCTCTCTCGACCTCAAGGGGACACCGCTGGGGCTGGGGCTGGGGCTGG	180	Db	1020 CTCCTGATCCAGACTCAAGCAGACCTGGGCTGGGGCTCTCTCTCTGGGT	1020
Db	121 CTCTCTCTCGACCTCAAGGGGACACCGCTGGGGCTGGGGCTGGGGCTGG	180	Db	1020 CTCCTGATCCAGACTCAAGCAGACCTGGGCTGGGGCTCTCTCTCTGGGT	1020
QY	181 GCTGGTGTCTACCTTGAGTGGGGCTGGGGCTGGGGCTGGGGCTGGGG	240	Db	1080 AACGACACATCTGCTAAAGAATGACTTGTTGTTGATTAATTTCCTTAT	1080
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QY	241 GCGGGGACGACGCCGGGGAGCTGGCTCTGGTACTCACCTCTGGGGGACT	300	Db	1140 AGCGAGTTCTACACTGGGGAGCTGGGAGCTGGGAGCTGGGAGCTGGGACT	1140
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QY	421 CTCACCGCTGGGGGGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	480	Db	1260 GTGGTAATAATAGGGGTATCACCAAGTTCTCAATAATTTCCCTTATAAAGGATT	1260
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QY	481 GTCGGGGGGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	540	Db	1320 GTCGTAATAATAGGGGTATCACCAAGTTCTCAATAATTTCCCTTATAAAGGATT	1320
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Db	541 GGCGGTGGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	600	Db	1380 GTCGCACTGG	1380
QY	601 CGCGACCGGAAATTGATTCGATTCGACACTGTTGCCACCATCTGGAGATTC	660	Db	1440 GGATCACCTGAGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1440
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QY	721 TACTCCAAATTTCAGATCAGAACCTCAAGGAGGACTCAGGTAGCTTC	780	Db	1560 1501 CTGGGGGGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1560
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QY	RESULT 2				
Db	ABQ81225				
QY	ID ABQ81226 standard; cDNA; 1743 BP.				
QY	AC ABQ81226;				
Db	XX				
Db	DT 05-DEC-2002 (first entry)				

XX DE Human 14273 nucleic acid, associated with metabolic disorder.

KW Human; 14273; metabolic disorder; obesity; diabetes; anorexia; cachexia; anorectic; antidiabetic; anabolic; transgenic animal; gene therapy; gene; BB.

XX OS Homo sapiens.

XX PN WO200267868-A2.

FH Location/Qualifier_B

Key 44 . 1.129

PT /*tag= a

FT /product= "14273"

XX PR 26-FEB-2001; 2001US-0271655P.

XX PA (MILL-) MILLENIUM PHARM INC.

PT Gimeno R, Tsai F;

XX DR WPI; 2002-698629/75.

DR P-PSDB; ABB79906.

XX PT Identifying a nucleic acid associated with a metabolic disorder, useful for diagnosing metabolic disorders, e.g. obesity, comprises contacting the sample with a probe comprising at least 25 contiguous nucleotides of the 14273 gene.

XX PS Claim 1; Fig 1A-B; 95PP; English.

CC The present sequence is that of a human nucleic acid, designated 14273, associated with metabolic disorders. 14273 molecules are expressed at high levels in adipose tissue, e.g. white adipose tissue and brown adipose tissue, as well as in pancreatic islets. They are upregulated during exposure to cold (i.e. under conditions that affect brown or white adipocyte metabolism) and downregulated in genetic models of obesity. 14273 knock-out mice, when fed a high-fat diet, gain more weight and have larger epididymal fat pads than wild-type mice. They also show increased levels of glucose and insulin upon fasting. A 14273 agonist may be beneficial to the treatment of obesity and/or type II diabetes by preventing fat accumulation on a high-fat diet and/or the increases in endogenous glucose production which occur in type II diabetes. The present invention provides 14273 nucleic acids, polypeptides and antibodies useful for the diagnosis and treatment of metabolic disorders including obesity, anorexia, cachexia and diabetes. Also provided are methods for identifying a subject having a metabolic disorder, for identifying a compound capable of modulating metabolic activity, methods for modulating metabolic activity (hypertrophic growth, hyperplastic lipogenesis or lipolysis in a subject, and a method for regulating endogenous glucose levels

XX SQ Sequence 1743 BP; 380 A; 479 C; 451 G; 433 T; 0 U; 0 Other;

Query Match 100.0%; Score 1743; DB 6; Length 1743;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1743; Conservative 0;

Oy 1 TCCGACTAGTCTGAGCCCTGGGGGCCAGCGCCGGGAGTCCTGATGCC 60

Dy 1 TCCGACTAGTCTGAGCCCTGGGGGCCAGCGCCGGGAGTCCTGATGCC 60

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1141 AGCCGAGTTCTCACACTGGGAGAGTGACAGAGTGCACTTCAGT 1200

1201 ACCCTCATCTGTCACCCCTTAAAGAAATGACCTATGCAAATAGACATCACAGC 1260

121 CTCTCTCCACGTCAGGGGACACCGCTGGCTCTGACGGGCTGGACACCGT 180

181 CCTGSGCTCTCTTGCAAGTGTGCTGCTGGCAAGGTGTTGGGCTGGCTGGC 240

181 GCTGGCTCTCTCTTGCAGTGTGCTGCTGGCAAGGTGAGCTGGCTGGC 240

241 GGGCGAGGAGCCGGGGGGAGCTGACTCTGACTGACTCTGGGGGACT 300

241 GGGCGAGGAGCCGGGGGGAGCTGACTCTGACTGACTCTGGGGGACT 300

301 GCTCTCATCGCGCTPATCCCCTGCTGGCTGGCTGGCTGGACTCTGCT 360

301 GCTCTCATCGCGCTPATCCCCTGCTGGCTGGCTGGACTCTGCT 360

361 GGGCCGTTCTGCTGCTGCTGGCTGGCTGGACTCTGCTGGACTCTGCT 420

361 GGGCCGTTCTGCTGCTGCTGGCTGGCTGGACTCTGCTGGACTCTGCT 420

421 CCTCAGCTGCGCTGCGCTGAGGAGCTGGCTGGCTGGACTCTGCT 480

421 CCTCAGCTGCGCTGCGCTGAGGAGCTGGCTGGCTGGACTCTGCT 480

481 CGTGGGGCTGCGCTGCGCTGAGGAGCTGGCTGGCTGGACTCTGCT 540

481 CGTGGGGCTGCGCTGCGCTGAGGAGCTGGCTGGACTCTGCT 540

541 GCGGGGGCCCTGCGCTGCGCTGGCTGGACTCTGCTGGACTCTGCT 600

541 GCGGGGGCCCTGCGCTGCGCTGGCTGGACTCTGCTGGACTCTGCT 600

601 CGCCGACCAGGAATTGATGATTCGACACTGATGGCCACATCTGGGATTC 660

601 CGCCGACCAGGAATTGATGATTCGACACTGATGGCCACATCTGGGATTC 660

661 GTGGGATGTCTTGTACTTGTGACTCTTGTGCCAGACTGTCATGTGATCG 720

661 GTGGGATGTCTTGTACTTGTGACTCTTGTGCCAGACTGTCATGTGATCG 720

721 TACTCCAATTTACAGATCACAAAGGCTCAGGAGGGCTACGGAGCTGG 780

721 TACTCCAATTTACAGATCACAAAGGCTCAGGAGGGCTACGGAGCTGG 780

781 CTACTGGAGGCCAACAGATGGCTGGCTGGAGGACTTCGGCTCTTGGACCT 840

781 CTACTGGAGGCCAACAGATGGCTGGCTGGAGGACTTCGGCTCTTGGACCT 840

841 CTTCCTCTCTGGTCTCTTCTCATCATCTGGAGGCCCTCATCATCACATCCCT 900

841 CTTCCTCTCTGGTCTCTTCTCATCATCTGGAGGCCCTCATCATCACATCCCT 900

901 CATCCGATCCAGAACTTCAGCAAGAACCTGGCTCATCTGGCTCTCTTGG 960

901 CATCCGATCCAGAACTTCAGCAAGAACCTGGCTCATCTGGCTCTCTTGG 960

961 GGTGGCTCTCATTTGCTTAACCCATCTCTACACAGACAGCTG 1020

961 GGTGGCTCTCATTTGCTTAACCCATCTCTACACAGACAGCTG 1020

1021 CAGGATGAGGAGAAATTTCAGGCTTCAACCCATCTCTACACAGACAGCTG 1080

1021 CAGGATGAGGAGAAATTTCAGGCTTCAACCCATCTCTACACAGACAGCTG 1080

1081 ACAGACATCTGTCAGAAAGAATGACTTCGATATTCTGGTATTTCTTAT 1140

1081 ACAGACATCTGTCAGAAAGAATGACTTCGATATTCTGGTATTTCTTAT 1140

1141 AGCCGAGTTCTCACACTGGGAGAAATTTCAGGAGTGACAGAGTGCACTTCAGT 1200

1141 AGCCGAGTTCTCACACTGGGAGAGTGACAGAGTGCACTTCAGT 1200

1201 ACCCTCATCTGTCACCCCTTAAAGAAATGACCTATGCAAATAGACATCACAGC 1260

QY	915	ACTCTTACGAAAGACCTGGTCATCCTGCCTCCCTCTCTGGGGGAGGCCCTCAT	974	PA (QUAN/)
PT	Smith KE, Quan Y;			XX
XX				
DR	WPI; 2003-198336/19.			XX
DR	P-PSDB; ABG73199.			XX
PT	New recombinant nucleic acid comprising a nucleic acid encoding a nucleic acid encoding a mammalian SNORF49 receptor, useful for screening antagonist to the SNORF49 receptor or as probes to obtain homologous nucleic acids from other species.			PT
DB	989 TGCCTATTGAGCCCTAACCCATCTACAGAATGACATGTGAGGAATGAGTGA 1048			PT
QY	1035 AGAAAATTGTTGCTCTGGTCCAGAAGGGAGCAATTAAACCCATCTACAGAATGACATGTGAGGAATGAGTGA 1094			PT
DB	1049 AGAAAATTGTTGCTCTGGTCCAGAAGGGAGCAATTAAACCCATCTACAGAATGACATGTGAGGAATGAGTGA 1108			PT
PS	Claim 2; Fig 1; 13pp; English.			PS
XX				XX
CC	The invention discloses a recombinant nucleic acid comprising a nucleic acid encoding a mammalian SNORF49 receptor, having a sequence identical to the sequence of the human SNORF49 receptor-encoding nucleic acid contained in plasmid pBxJ-T73BS-HS-SNORF49. SNORF49 receptor is a neuromodulator. The nucleic acid is useful for expressing the receptor in transfected cells, for screening for antagonists to the SNORF49 receptor or as probes to obtain homologous nucleic acids from other species and to detect the existence of nucleic acids having complementary sequences in samples. The receptor can also be used in the design of drugs for treating various pathophysiological conditions, such as inflammation, arthritis, autoimmune disease, transplant rejection, infections, septicemia, AIDS, neurological disorders, such as schizophrenia and epilepsy, respiratory disorders, asthma, obesity, diabetes, anorexia, cardiovascular disorders, ischaemia, stroke, cancer, sexual/reproductive disorders, circadian rhythm disorders, renal disorders, bone diseases, osteoporosis, allergy, Parkinson's disease and Alzheimer's disease. The sequence presented is the DNA encoding the human orphan SNORF49 receptor.			CC
CC	Sequence 1160 BP; 192 A; 372 C; 318 G; 278 T; 0 U; 0 Other;			CC
QY	Query Match 63.6%; Score 1109; DB 7; Length 1160; Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0; Matches 1159; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			QY
DB	1395 CAGGAGTTGAGGACCACTGACCAACATGGTAGGGAGGCTGGAGGTACCTGAGT 1444			QY
DB	1409 CAGGAGTTGAGGACCACTGACCAACATGGTAGGGAGGCTGGAGTACCTGAGT 1458			QY
RESULT 4				QY
ABX10627				17 ACGCTTGAGGGGCCACGGCGGGGAATGTCCTGATGCGCGGGCACGGCGAC
ID	ABX10627 standard; DNA; 1160 BP.			76 1 ACCCTGGGGGCCACGGCGGGGAATGTCCTGATGCGCGGGCACGGCGAC
XX				60 77 GCGCCCTTGGCGACCTGGAGGAGACGCCACCGCTTCCCTTCTCCGACCTC
AC				136 61 GCGCCCTTGGCGACCTGGAGGAGACGCCACCGCTTCCCTTCTCCGACCTC
XX				120 137 AAGGGGACCAAGGGCTGGCTGGCCGGGGAGAACCTGGCTGGCTCATCTT
DT	ABX10627;			196 121 AAGGGGACCAAGGGCTGGCTGGCCGGGGAGAACCTGGCTGGCTCATCTT
XX				180 197 GCGAGTGCTGGCTGGCCGGGGAGAACCTGGCTGGCTGGCTGGCTCATCTT
DE	11-APR-2003 (first entry)			256 181 GCGAGTGCTGGCTGGCCGGGGAGAACCTGGCTGGCTGGCTGGCTCATCTT
XX				240 257 GCGGGACTGGCTGGCTGGTACCTCTGGGGAGCTGGCTGGCTGGCTGGCT
DNA	encoding human orphan SNORF49 receptor.			316 241 GGGGGACTGGCTGGCTGGCTGGTACCTCTGGGGAGCTGGCTGGCTGGCT
XX				300 317 ATCCCTCTGGCTGGCTGGCTGGTACCTCTGGGGAGCTGGCTGGCTGGCT
OS	Human; gene; db; SNORF49 receptor; neuroregulator; inflammation; arthritis; autoimmune disease; transplant rejection; infection; septicemia; AIDS; neurological disorder; schizophrenia; epilepsy; respiratory disorder; asthma; obesity; diabetes; anorexia; cardiovascular disorder; ischaemia; stroke; cancer; sexual disorder; reproductive disorder; circadian rhythm disorder; renal disorder; bone disease; osteoporosis; allergy; Parkinson's disease; Alzheimer's disease.			376 301 ATCCCTCTGGCTGGCTGGCTGGTACCTCTGGGGAGCTGGCTGGCTGGCT
KX	Homo sapiens.			360 377 CACCTGCTCTTACGTCATGACCACTGGCTGGCTGGCTGGCTGGCTGGCT
FH	Key Location/Qualifiers			416 361 CACCTGCTCTTACGTCATGACCACTGGCTGGCTGGCTGGCTGGCTGGCT
FT	28 .1113			420 437 GTGAGCTTGGAGGAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT
FT	/*tag= a /product= "SNORF49 receptor"			496 421 GTAGGCTTGGAGGAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG
XX	US2002151705-A1.			540 497 CGCGGGGGAGGAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG
XX	17-OCT-2002.			556 481 CGCGGGGGAGGAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT
XX	11-DEC-2001; 2001US-00015498.			540
XX	05-OCT-1999; 99US-00412933.			
XX	(SMITH/) SMITH K E.			
PA				

PF	07-DEC-2000; 2000WO-US033398.
XX	10-DEC-1999; 99US-0172852P.
PR	22-DEC-1999; 99US-017172P.
PR	14-JAN-2000; 2000US-017618P.
PR	21-JAN-2000; 2000US-017731P.
XX	(INCY-) INCYTE GENOMICS INC.
PA	Burford N., Baughn MR., Au-Young J., Yang J., Lu DAM., Reddy R.,
PI	WPI; 2001-381635/40.
XX	P-PSDB; AABE4564.
DR	
Db	824 CGGCTCTCGAACCTCTCCCTCATGGTCTCTCATGTGGAGGCCACAGATCGGCTGTCACAGGGACTC 823
Db	721 CTCAGCTGAGCTGCTACTGGAGAGGCCACAGATCGGCTGTCACAGGGACTC 780
Db	841 ATCATCACCATCCCTCATGGTCTCTCATGTGGAGGCCACAGATCGGCTGTCACAGGGACTC 883
Db	781 CGCTCTCGAACCTCTCCCTCATGGTCTCTCATGTGGAGGCCACAGATCGGCTGTCACAGGGACTC 840
Qy	944 TCCTCTCTCGGGTGGCTCACATTGCTTAITCGCTTAACCCATCTC 1003
Db	901 TCCCTCTCTCGGGTGGCTCACATTGCTTAITCGCTTAACCCATCTC 960
Db	1004 TACAAACATGACACTGTCAGGAATGGTGGAGAAATTGGCTGCTCTGGTCCA 1063
Db	961 TACAAACATGACACTGTCAGGAATGGTGGAGAAATTGGCTGCTCTGGTCCA 1020
Qy	1064 GAAAAGGAGCCATTAAAGACAATCTGTCAAAGAAATTTGGCTGCTCTGGTCCA 1123
Db	1021 GAAAAGGAGCCATTAAAGACAATCTGTCAAAGAAATTTGGCTGCTCTGGTCCA 1080
Qy	1124 GGCTAA 1129
Db	1081 GGCTAA 1086
RESULT 6	
AAD08854	Human G-protein coupled receptor-20 (GCRBC-20) cDNA.
ID	AAD08854 standard; cDNA; 1321 BP.
XX	
AC	
AAD08854;	
XX	
DT	04-SEP-2001 (first entry)
XX	
DE	Human G-protein coupled receptor-20 (GCRBC-20) cDNA.
KW	Human; G-protein coupled receptor-20; GCRBC-20; gene therapy; cirrhosis; transgenic animal; proliferative disorder; actinic keratosis; hepatitis nephrotropic; cancer; breast; bladder; bone marrow; brain; uterus; leukaemia; adenocarcinoma; lymphoma; melanoma; myeloma; epilepsy; stroke; neurological disorder; Alzheimer's disease; Huntington's disease; Addison's disease; allergies; anaemia; asthma; diabetes mellitus; atopic dermatitis; glomerulonephritis; Grave's disease; osteoarthritis; fungal; proriasis; rheumatoid arthritis; ulcerative colitis; bacterial; parasitic; protozoal and helminthic infections; and metabolic disorders (obesity, osteoporosis, viral infections).
XX	
Query Match	Sequence 1321 BP; 243 A; 404 C; 348 G; 326 T; 0 U; 0 Other; Best Local Similarity 99.8%; Pred. No. 0; Mismatches 0; Length 1321; Matches 1181; Conservative 0; Gaps 0;
Qy	32 CAGCGCGGGATGCCCTGATGGGGGAGCGGGAGCGCCCTTGCGAGC
Db	18 CAGCGCGGGATGCCCTGATGGGGGAGCGGGAGCGCCCTTGCGAGC 77
Qy	92 CTCGAGCAGCCACCGCCGCTTCCCTCTCGAGTCAGGGCCACCGG 151
Db	78 CTGAGCAGCCACCGCCGCTTCCCTCTCGAGTCAGGGCCACCGG 137
Qy	152 CTGGTGTGGCCGGGGTGGAGAGCACCGTGTGGTGTCACTTGGAGTGTGGCTCTG 211
Db	138 CTGGTGTGGCCGGGGTGGAGAGCACCGTGTGGTGTCACTTGGAGTGTGGCTCTG 197
Qy	212 GCGAACCTGGCCGGCTGGTGTGGAGAGCACCGTGTGGTGTCACTTGGAGTGTGGCTCTG 271
Db	198 GCGAACCTGGCCGGCTGGTGTGGAGAGCACCGTGTGGTGTCACTTGGAGTGTGGCTCTG 257
FT	272 CTGGTGTGGCCGGGGTGGAGAGCACCGTGTGGTGTCACTTGGAGTGTGGCTCTG 331
FT	258 CTGGTGTGGCCGGGGTGGAGAGCACCGTGTGGTGTCACTTGGAGTGTGGCTCTG 317
PN	WO200142288-A2.
XX	14-JUN-2001.
PD	
XX	
Key	Location/Qualifiers
CD5	30...1115
/*tag=	a
/product=	"Human GCRBC-20 protein"

	361	AGCGCAGGCTCACCACTCACGCCCTACGGGGCCAGCTGGAGCGATGTGCATC	420	os	Homo sapiens.
464	GTCACCTCGACGCCGCGCGAGCTCGGGCTCGCTCTCGGTCTCGGTCTCGTGGCG	523	XX	Key	Location/Qualifiers
421	GTGCACTCGACGCCGCGCGAGCTCGGGCTCGCTCTCGGTCTCGGTCTCGTGGCG	480	FT	CDS	1. .1086
524	CTCTCTGGGCTATCGGGGTCGGCTCGCTCTCGGTCTCGGTCTCGTGGCG	583	FT		/*tag= b
481	CTCTCTGGGCTATCGGGTCCCGCTCGCTCTCGGTCTCGTGGCG	540	FT		/product= "HGPRBMY18"
584	CCGACCGCTCCCCGGCGCGACAGGAATTGATGTTGACACTGATTTGGCCACC	643	FT		/transl_except= (pos:364..372,aa:Gly-Val)
541	CCGACCGCTCCCCGGCGCGACAGGAATTGATGTTGACACTGATTTGGCCACC	600	FT		1. .1083
644	ATTCCTGGAGAGATCTCGTGGATCTCTCTTGACTTTGAACTCTTGTGCGAGGA	703	PN		/*tag= a
601	ATTCTCTGGAGAGATCTCGTGGATCTCTCTTGACTTTGAACTCTTGTGCGAGGA	660	XX		/note= "Claimed in claim 1"
704	CTGGCTATGAGACTCTCCAAATTAGTACAGTACAAGAACATCAGGAGAGG	763	XX		4. .1083
661	CTGGCTATGAGACTCTCCAAATTAGTACAGTACAAGAACATCAGGAGAGG	720	PR		/*tag= c
764	CTCAGGTAAGCCTGCTACTCGAGAGCCACCGATCCCGTCTCCAGAGACTC	823	PR		/note= "Claimed in claim 1"
721	CTCAGGTAAGCCTGCTACTCGAGAGCCACCGATCCCGTCTCCAGAGACTC	780	PA		
824	CGGCTTCCGACACTCTCTCTCTCTCTCATGTCAGGAGCTGGTGTATCGGCC	883	PA		
781	CGGCTTCCGACCTCTCTCTCTCATGTCATCGAGCCCATC	840	PA		
884	ATCTTACCATCCCTCATCTGATCCAGACTCTGGAGCCACGATCCCGTCTCC	943	PI		(FEDE/) FEDER J N.
QY	ATCTTACCATCCCTCATCTGATCCAGACTCTGGAGCCACGATCCCGTCTCC	900	PA		(MINT/) MINTIER G.
Db	ATCTTACCATCCCTCATCTGATCCAGACTCTGGAGCCACGATCCCGTCTCC	960	PA		(RMA/) RAMANATHAN C S.
944	TCCCTCTCTCTGGTGGGGCTCACATTGTTGCTCTTCTCTCTCTCTCTCT	1003	PA		(HAWK/) HAWKEN D R.
901	TCCCTCTCTCTGGTGGGGCTCACATTGTTGCTCTTCTCTCTCTCTCTCT	960	XX		
904	TACACATGACACTCTGAGGAATGTTGCTCTTCTCTCTCTCTCTCTCTCT	1063	DR		
961	TACACATGACACTCTGAGGAATGTTGCTCTTCTCTCTCTCTCTCTCTCT	1020	XX		
QY	1064 GAAGGGGACCATTTAACAGACATCTGTCATAAGAATGACTGTCGATTCT	1123	PT		P-PTDB; ADB47642.
Db	1021 GAAGGGGACCATTTAACAGACATCTGTCATAAGAATGACTGTCGATTCT	1080	PT		
QY	1124 GGCTAA 1129		PT		
Db	1081 GGCTAA 1086		PT		
RESULT 9			XX		
ADB47641	ID	ADB47641 standard; cDNA; 1086 BP.	PS		Claim 1; 71pp; English.
AC	AC	ADB47641;	XX		The invention relate to an isolated human G protein-coupled receptor
XX	XX		CC		(GPCR), HGPRBMY18, polynucleotide encoding a novel human GPCR HGPRBMY18.
XX	XX		CC		Also included are expression vectors, host cells, a fusion protein
XX	XX		CC		comprising HGPRBMY18 and an FC portion of a human immunoglobulin protein,
XX	XX		CC		an anti-HGPRBMY18 antibody its antigenic epitope, screening a library of
XX	XX		CC		molecules or compounds with a polynucleotide to identify at least one
XX	XX		CC		molecule or compound which specifically binds to the polynucleotide
XX	XX		CC		sequence and screening for candidate compounds capable of modulating
XX	XX		CC		activity of a G-protein coupled receptor-encoding polypeptide. HGPRBMY18
XX	XX		CC		or its (anti)agonist (small molecule, peptide, and antisense molecule) is
XX	XX		CC		useful for treating a disease, disorder, or condition related to the
XX	XX		CC		endocrine, gastrointestinal, reproductive, pulmonary, or neural system.
XX	XX		CC		Diseases include endocrine disorders, disorders of the pituitary,
XX	XX		CC		aberrant growth hormone synthesis and/or secretion, aberrant prolactin
XX	XX		CC		synthesis and/or secretion, aberrant sexual characteristic development,
XX	XX		CC		secretion, aberrant follicle-stimulating hormone synthesis and/or
XX	XX		CC		secretion, aberrant thyroid-stimulating hormone synthesis and/or
XX	XX		CC		secretion, aberrant adrenocorticotropin synthesis and/or secretion,
XX	XX		CC		aberrant lactation, aberrant sexual characteristic development, aberrant
XX	XX		CC		testosterone synthesis and/or secretion, aberrant water homeostasis, hypogonadism,
XX	XX		CC		synthesis and/or secretion, aberrant water homeostasis, hypogonadism,
XX	XX		CC		addison's disease, hypothyroidism, cushing's disease, agromegaly,
XX	XX		CC		follicle-stimulating hormone, thyroid-stimulating hormone;
XX	XX		CC		adrenocorticotropin, vasopressin; oxytocin; aberrant growth;
XX	XX		CC		aberrant lactation; aberrant sexual characteristic development;
XX	XX		CC		testosterone; oestrogen; aberrant water homeostasis; hypogonadism;
XX	XX		CC		addison's disease; hypothyroidism; cushing's disease; agromegaly;
XX	XX		CC		giantism; lethargy; osteoporosis; aberrant calcium homeostasis;
XX	XX		CC		aberrant potassium homeostasis; reproductive disorder;
XX	XX		CC		developmental disorder; colon cancer; breast cancer; prostate cancer;
XX	XX		CC		related proliferative condition of the breast, prostate cancer, related
XX	XX		CC		proliferative condition of the breast, prostate cancer, related

QY	1164	GAAGGGAGCATTACAGACATCTGTCAGAAATTTTGCTCTTGTTCCA	1063
Db	1021	GAGGGAGCCATTACAGACATCTGTCAGAAATTTTGCTCTTGTTCCA	1123
Db	1124	GGCTAA 1129	
Db	1081	GGCTAA 1086	
			1080
RESULT 10			
ID	ABS73399	standard; DNA; 1086 BP.	
ID	ABS73399		
AC	ABS73399;		
XX			
DT	04-DEC-2002	(first entry)	
XX			
DE	DNA encoding human GPCR HF1948 mutant E135N.		
XX			
KW	Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy; hypertension; reflux disease; depression; migraine; schizophrenia; ulcer; psychotropic disorder; asthma; bronchospasm; anaesthesia; myocardial infarction; MI; stroke; glaucoma; anxiety; prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina; prostatic hypertrophy; mutant; ds; OS		
XX			
OS	Homo sapiens.		
XX			
PN	W0200268600-A2.		
XX			
PD	06-SEP-2002.		
XX			
PF	26-FEB-2002; 2002WO-US005625.		
XX			
PR	26-FEB-2001; 2001US-0271913P.		
XX			
PA	(AREN-) ARENA PHARM INC.		
XX			
PI	Lilaw CW, Chalmers DT, Behan DP, Maciejewski-Lenior D, Leonard JN;		
PI	Lin I, Ortuno D;		
XX			
DR	WPI; 2002-706980/76.		
DR	P-PADB; ABG95170.		
XX			
PT	New human G-protein coupled receptor (GPCR), useful for screening agonist or inverse agonist compounds for treating diseases associated with GPCR.		
PT			
PS	Example 2; Page 183; 201pp; English.		
XX			
CC	The present invention relates to transmembrane receptors, particularly endogenous human G-protein coupled receptors (GPCRs), mutant (non-endogenous) versions of the GPCRs, and the polynucleotide sequences encoding them. The GPCRs are useful for screening agonist or inverse agonist compounds for treating diseases associated with GPCR. Diseases can be treated with such compounds include allergies, hypertension, reflux disease, depression, migraine, schizophrenia, ulcers, psychotropic disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI), stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer, anxiety, prostatic hypertrophy, rhinitis, and angina. The present sequence encodes a mutant human GPCR.		
CC			
CC			
SQ	Sequence 1086 BP; 183 A; 348 C; 293 G; 262 T; 0 U; 0 Other;		

				KW
231	TGCTGTGGGGGCGACAGAGCCGGGGGCGACTGCCTCTTCAACCTCTCT	247	XX	diagnosis; treatment; receptor-mediated disorder; screening;
291	GCGGACCTGCTCTCATCAGCCTATCCCTCTGTGTGGCCGTGCTGAACTGAG	350	OS	Homo sapiens.
248	GCGGACCTGCTCTCATCAGCCTATCCCTCTGTGTGGCCGTGCTGAACTGAG	307	XX	location/Qualifiers
QY			XX	44..1129
Db			XX	/tag= a
Db			XX	/product= "Human 14273 G-Protein coupled receptor"
351	CCTCGCTCTGGACCCGTTGCCACCTGCTCTTGCTGTGAGTCAGGCTGGGCA	410	XX	receptor and somatostatin"
308	CCTCGCTCTGGACCCGTTGCCACCTGCTGTGAGTCAGGCTGGGCA	367	XX	/transl_except= (pos:353..355, aa:Tyr)
411	GGCTTACCTCTCAAGCTGGCTGGGGTAGCTGGCTGGGGCATGGTGTGAG	470	XX	/transl_except= (pos:467..469, aa:Met)
368	GCGTACCATCTCTCAAGCTGGCTGGGGCATGGTGTGAG	427	XX	/transl_except= (pos:488..490, aa:Cys)
471	TGGAGCGGG	530	XX	/transl_except= (pos:494..496, aa:Cys)
428	TGAGCGGG	487	XX	/transl_except= (pos:494..535, aa:Gly)
QY			XX	/transl_except= (pos:494..533, aa:Gly)
Db			XX	/transl_except= (pos:494..533, aa:Gly)
Db			XX	/transl_except= (pos:494..535, aa:Gly)
QY			XX	/transl_except= (pos:494..535, aa:Gly)
Db			XX	/transl_except= (pos:494..535, aa:Gly)
QY			XX	/transl_except= (pos:494..535, aa:Gly)
QY			XX	/transl_except= (pos:494..535, aa:Gly)
531	GGCCCTATTGGGGGTCGGCTCTGCCCTCTGGCTGAGCTGCTCCGAC	590	XX	/transl_except= (pos:494..535, aa:Gly)
488	GGGGTATTGGGGTCGGCTCTGCCCTCTGGCTGCTCCGAC	547	XX	/transl_except= (pos:494..535, aa:Gly)
591	GGCTCCCCGGGGGACCGGAAATTGCAATTGCACTGATTTGGCCACATTCTC	650	XX	/transl_except= (pos:788..790, aa:Thr)
548	GGCTCCCCGGGGGACCGGAAATTGCAATTGCACTGATTTGGCCACCTCTC	607	XX	/transl_except= (pos:788..790, aa:Thr)
651	GAGAGATCTGTGGATGCTTGTGACTTGTGACTTGTGATTTGGCCAGGTGCA	710	XX	/transl_except= (pos:791..793, aa:Ser)
QY			XX	/transl_except= (pos:791..793, aa:Ser)
Db			XX	/transl_except= (pos:887..889, aa:Asp)
Db			XX	/transl_except= (pos:950..952, aa:Cys)
Db			XX	/transl_except= (pos:953..955, aa:Pro)
Db			XX	/transl_except= (pos:965..967, aa:Ala)
Db			XX	/transl_except= (pos:968..970, aa:Pro)
QY			XX	458..460
Db			XX	/tag= b
Db			XX	/note= "Encodes Cys"
Db			XX	464..466
Db			XX	/tag= C
Db			XX	/note= "Encodes Val"
608	GAGAGATCTGTGGATGCTTGTGACTTGTGATTTGGCCAGGTGCA	667	XX	
711	TGCTGATCAGTACTCCAAAATTTACAGATCACAAAGCATCAGGAGAGCTACGG	770	XX	
668	TGCTGATCAGTACTCCAAAATTTACAGATCACAAAGCATCAGGAGAGCTACGG	727	XX	
QY			XX	
771	TAACCTGGCTACTGGAGAACCCAGATCCGGGTGTCGCCAGAGGACTTCGGCT	830	XX	
728	TAAGCTGGCTACTGGAGAACCCAGATCCGGGTGTCGCCAGAGGACTTCGGCT	787	XX	
831	TCCGACCCCTCTCTCCCTCATGGTCTCTCTCATGTGCGGCCCATCATCATCA	890	XX	
788	TCCGACCCCTCTCTCTCATGGTCTCTCATGTGCGGCCCATCATCATCA	847	XX	
QY			XX	
891	CCATCTCTCATCTGATCCAGAACCTCAAGAGAATCTGCTCATCGGCCCTCT	950	XX	
848	CCATCTCTCATCTGATCCAGAACCTCAAGAGAATCTGCTCATCGGCCCTCT	907	XX	
QY			XX	
951	TCTCTGGGGGGCTCACATTGCTATTGAGCCCTAACCCCATCTCACACA	1010	XX	
908	TCTCTGGGGGGCTCACATTGCTATTGAGCCCTAACCCCATCTCACACA	967	XX	
QY			XX	
1011	TGACATGTGGCAGGATGAGTGGAGAAATTGCTGCTCTGGTCCAGAAGAG	1070	XX	
Db			XX	
968	TGACATGTGGCAGGATGAGTGGAGAAATTGCTGCTCTGGTCCAGAAGAG	1027	XX	
QY			XX	
1071	GAGCATTAAACAGACATCTGCTAACAAAAGAATGACTTGCTGATTTCTGCTAA	1129	XX	
Db			XX	
1028	GAGCATTAAACAGACATCTGCTAACAAAAGAATGACTTGCTGATTTCTGCTAA	1086	XX	
RESULT 12			XX	
AAZ4945			XX	
AAZ4945 standard; cDNA; 1742 BP.			XX	
AAZ4945;			XX	
XX			XX	
DT			XX	
02-MAY-2000 (first entry)			XX	
DE			XX	
Human 14273 G-protein coupled receptor (GPCR) encoding cDNA.			XX	
G-protein coupled receptor; GPCR; 14273 receptor; human; somatostatin; cellular function/activity; galanin receptor; chemokine receptor; AC			XX	
AAZ4945;			XX	
XX			XX	
02-MAY-2000			XX	
Query Match	52.4%		XX	
Best Local Similarity	99.1%		XX	
Matches	1613; Conservative		XX	
Score	913; DB 3;		XX	
Length	1742;		XX	
Mismatches	0;		XX	
Indels	0;		XX	
Gaps	0;		XX	
Gap	0;		XX	

PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214888P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0215647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217958P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 14-AUG-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
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 PR 18-AUG-2000; 2000US-0226219P.
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 PR 13-OCT-2000; 2000US-023935P.
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 PR 08-DEC-2000; 2000US-0251900P.
 PR 11-DEC-2000; 2000US-0254057P.
 PR 05-JAN-2001; 2001US-0259678P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX
 PR Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-541565/60.
 XX
 PR Nucleic acids encoding 3224 human nervous system antigen polypeptides'
 PR useful for preventing, diagnosing and/or treating nervous system cancers
 PR and metastases.
 XX Disclosure; SEQ ID NO 13763; 1701pp + Sequence Listing; English.
 XX The invention relates to novel genes (ABN1004-ABN21534) and proteins
 CC (ABB1678-BBB1801) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are

CC isolated from a range of human tissues disclosed in the specification.

CC The nucleic acids, proteins, antibodies and (anti)agonists are useful in CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune CC disorders e.g. Addison's disease, allergies, anaemia, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) CC cardiovascular disorders such as myocardial ischaemias, (d) wound healing ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) CC infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published/pct_sequences

XX SQ Sequence 746 BP; 224 A; 149 C; 164 G; 209 T; 0 U; 0 Other;

Best Local Similarity 42.8%; Score 746; DB 5; Length 746; Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 976 TGCTTAATTGAGGCCAAACCCATCCTCACACATGACACTGGCAGGAAGTGGAA 1035

Db 1 TGCATAATTGAGGCCAAACCCATCCTCACACATGACACTGGCAGGAAGTGGAA 60

QY 1036 GAAAATTTTGCTGCTTGCTGTGTCAGAACGGGCCATTAAACAGACCATGT 1095

Db 61 GAAATTGTTTGCTGCTTGCTGTGTCAGAACGGGCCATTAAACAGACCATGT 120

QY 1096 CAAAAGAAATGACTGTGATGATATTTCGGCAATTTCCTTATASCGGAGTTCTAC 1155

Db 121 CAAAAGAAATGACTGTGATGATATTTCGGCAATTTCCTTATASCGGAGTTCTAC 180

QY 1156 ACCTGGCGAGCTGGCATGCTTTAACAGAGTCATTCCGTAACCTCCATCAGTGC 1215

Db 181 ACCTGGCGAGCTGGCATGCTTTAACAGAGTCATTCCGTAACCTCCATCAGTGC 240

QY 1216 ACCCTGCTTAGAAGATGAACTATGCAAATAGACATCCCAAGCGTGGTAATTAGG 1275

Db 241 ACCCTGCTTAGAAGATGAACTATGCAAATAGACATCCCAAGCGTGGTAATTAGG 300

QY 1276 GTGTATCAGCAAGTTCAATTATTCCTTAAAGGATTGTTGGCCAGGTGGCAG 1335

Db 301 GTGTATCAGCAAGTTCAATTATTCCTTAAAGGATTGTTGGCCAGGTGGCAG 360

QY 1336 TGGTCATCCGTAATCCAGCGTTRGGAGCTGGTGGGGCTGGATCACTGAGTC 1395

Db 361 TGGTCATCCGTAATCCAGCGTTRGGAGCTGGTGGGGCTGGATCACTGAGTC 420

QY 1396 AGGAGTCAGACCAACTGACACATGGAGACCCCGCTCTACTAAATAAAA 1455

Db 421 AGGAGTCAGACCAACTGACACATGGAGACCCCGCTCTACTAAATAAAA 480

QY 1456 AAAAATATTAGCTGGAGTGGTGGGGACCTGTAATCTAGTACTTGGAGCTGAC 1515

Db 481 AAAAATATTAGCTGGAGTGGTGGGGACCTGTAATCTAGTACTTGGAGCTGAC 540

QY 1516 CAGCGAACTCTTGAACTTGGGGAGAGTGGAGCTGGAGAGTGTGCAATGGC 1575

Db 541 CAGCGAACTCTTGAACTTGGGGAGAGTGGAGCTGGAGAGTGTGCAATGGC 600

QY 1576 ACTCCACCAAGGGCAACAGTGAACTCCATTAAGAAAAAAAGATCT 1635

Db 601 ATCCACCAAGGGCAACAGTGAACTCCATTAAGAAAAAAAGATCT 660

QY 1636 TATGGTTCTTAAATGTCAGCTTAACTTGTGTTGTTAATATGTCATAATTAA 1695

Db 661 TATGGTTCTTAAATGTCAGCTTAACTTGTGTTGTTAATATGTCATAATTAA 720

QY 1696 ATATTTATTTAGTACTGTGCAAGA 1721

Db 721 ATATTTATTTAGTACTGTGCAAGA 746

XX SQ Sequence 632 BP; 219 A; 113 C; 134 G; 166 T; 0 U; 0 Other;

Best Local Similarity 33.6%; Score 586; DB 7; Length 632; Matches 586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1130 TTTTCTTATAGCCGAGTTCTCACACTGGAGCTGGAGCTTAAACAGT 1189

Db 1 TTTCCTTATAGCCGAGTTCTCACACTGGAGCTGGAGCTTAAACAGT 60

QY 1190 TCATTCAGTACCTCCATCAGTCACCTGGAGCTTAAAGAATGACACTGCAATAG 1249

Db 61 TCATTCAGTACCTCCATCAGTCACCTGGAGCTTAAAGAATGACACTGCAATAG 120

OY	1250 ACATCCACAGCGTCGTAATTAAAGGGTATCACCAAGTTTACATATTTCCCTTA	1309
DR	DB	XX
XX	121 ACATCCACAGCGTCGTAATTAAAGGGTATCACCAAGTTTACATATTTCCCTTA	180
PT	1310 TAAGGATTGTGCGGACGGTGCAGGTCACTCTGATTCAGGTTGGAGG	1369
PT	181 TAAGGATTGTGCGGACGGTGCAGGTCACTCTGATTCAGGTTGGAGG	240
PT	OY	QY
PS	QY	QY
XX	1370 CTGAGGGGGGATCACCTGAGGTGAGGTTGGAGG	1429
CC	DB	241 CTGAGGGGGGATCACCTGAGGTGAGGTTGGAGG
CC	CC	300
CC	1430 ACCCCGTTCTACTAAATAAAAAAATTGCTGGAGTGCTGGGACCTGT	1489
CC	301 ACCCCGTTCTACTAAATAAAAAAATTGCTGGAGTGCTGGGACCTGT	360
CC	421 GCAGTAGGCCGATGTGCCCCATCTAACGGGACAGAGTCCATC	480
CC	OY	QY
CC	1490 AACCTCTAGTACTGGGAGCTGAAACCAGGAACTCTGGAGGCAAGGGT	1549
CC	361 AACCTCTAGTACTGGGAGCTGAAACCAGGAACTCTGGAGGCAAGGGT	420
CC	Db	1550 GCAGTAGGCCGAGATGCTGGGACAGAGTGAACCTCATC
CC	CC	1609
CC	421 GCAGTAGGCCGATGTGCCCCATCTAACGGGACAGAGTCCATC	480
CC	OY	QY
CC	1610 TAAAGAAAAGAAAAGATTGTTAGGGTCTTAAATGACTGT	1669
CC	481 TAAAGAAAAGAAAAGATTGTTAGGGTCTTAAATGACTGT	540
CC	Db	1670 TGTGTTGTAATGATCAAAATTAAATTTATGACTGT
CC	541 TGTGTTGTAATGATCAAAATTAAATTTATGACTGT	586
CC	OY	QY
CC	541 TGTGTTGTAATGATCAAAATTAAATTTATGACTGT	586
CC	RESULT 15	
AC	ADB4744 standard; cDNA; 632 BP.	
AC	ADB4744;	
XX	ADB4764;	
XX	04-DEC-2003 (first entry)	
XX	Human cDNA encoding GPRM18, 3' UTR.	
XX	KW Human; ss; gene; G protein-coupled receptor; GPCR; endocrine disorder; pituitary disorder; growth hormone; prolactin; luteinizing hormone; follicle-stimulating hormone; thyroid stimulating hormone; adrenocorticotropin; vasopressin; oxytocin; aberrant growth; aberrant lactation; aberrant sexual characteristic development; aberrant testosterone synthesis and/or secretion; aberrant follicle-stimulating hormone synthesis and/or secretion; aberrant thyrotropin-stimulating hormone synthesis and/or secretion; aberrant vasopressin secretion; aberrant oxytocin secretion; growth, aberrant lactation, aberrant sexual characteristic development, aberrant testosterone synthesis and/or secretion; aberrant oestrogen synthesis and/or secretion; aberrant water homeostasis; hypogonadism, Addison's disease; hypothyroidism, Cushing's disease; agenitalia, gigantism, lethargy, osteoporosis, aberrant calcium homeostasis, aberrant potassium homeostasis, reproductive disorders, developmental disorders, colon cancer, related proliferative condition of the colon, breast cancer, related proliferative condition of the breast, prostate cancer, related proliferative condition of the prostate, lung cancer, and related proliferative condition of the lung. In addition, determining the presence or amount of expression of HGRPM18 is useful for diagnosing a susceptibility to a pathological condition such as colon cancer, related proliferative condition of the breast, prostate cancer, related proliferative condition of the prostate, lung cancer, and related proliferative condition of the lung. The present sequence represents the 5' or 3' UTR of the cDNA encoding HGRPM18.	
XX	SQ Sequence 632 BP; 219 A; 113 C; 134 G; 166 T; 0 U; 0 Other; Query Match 33.6%; Score 586; DB 8; Length 632; Best Local Similarity 100.0%; Pred. No. 3.5e-16; Matches 586; Conservative 0; Mismatches 0; Indels 0; Gaps 0; CC	
XX	OY 1130 TTTCTTATACCGAGTTCTCACCTCTGGCAGCTGCTGTTAACAGAST 1189	
XX	1. TTTCTTATACCGAGTTCTCACCTCTGGCAGCTGCTGTTAACAGAST 1189	
DB	Db	1. TTTCTTATACCGAGTTCTCACCTCTGGCAGCTGCTGTTAACAGAST 60
QY	QY	1190 TCATTCAGTACCTCCATCAGTCACCTGCTTAAGAAATGACCTATGAAATG 1249
DB	Db	61 TCATTCAGTACCTCCATCAGTCACCTGCTTAAGAAATGACCTATGAAATG 120
OY	OY	1250 ACATCCACAGCGTCGTAATTAAAGGGTATCACCAAGTTCAATATTCCTTA
PA	PA	1250 ACATCCACAGCGTCGTAATTAAAGGGTATCACCAAGTTCAATATTCCTTA
PA	PA	121 ACATCCACAGCGTCGTAATTAAAGGGTATCACCAAGTTCAATATTCCTTA
PA	PA	1310 TAAGGATTGTGCGGACGGTGCAGGTGCTCATGCCGTAATCCAGCGTTGGAGG
PA	PA	14-Nov-2001; 2001US-00992331.
XX	XX	181 TAAGGATTGTGCGGACGGTGCAGGTGCTCATGCCGTAATCCAGCGTTGGAGG
(FEDE/)	FEDER J N.	240
PA	PA	1370 CTGAGGGGGGATCACCTGAGGTGAGGTTGGAGG
(MINT/)	MINTER G.	1429
PA	PA	14-Nov-2001; 2001US-00992331.
(RAMA/)	RAMANTHAN C S.	
PA	PA	(HAWK/)
XX	XX	HAWKEN D R.

us-10-077-698-2.oligo904.rng

OY	1430	ACCCCCGGTCTACTCTAAAGATATAAAGAAAATTAGCTGGGAGCTGGTGGGCCACCTGT	1489
Db	301	ACCCC CGTCTACTCTAAAGATATAAAGAAAATTAGCTGGGAGCTGGTGGGCCACCTGT	360
OY	1490	AATCC TACTACTTG GAGGTCAAC CAGGAGATCTCTGACCTGGAGGCAGGGTT	1549
Db	361	AATCC TAGCTACTGTGGAGGCTGACCCAGGAGATCTTGACCTGGAGGAGGAGGT	420
Oy	1550	GCAGT GAGCC GAGAT CTG GCC ATG CACT CC AACCS GG CAAC AA GAGT GAA CCT ATC	1609
Db	421	GCAGT GAGCC GAGAT CTG GCC ATG CACT CC AACCC AGGG CAAC AA GAGT GAA ACT CC ATC	480
Oy	1610	TAA AAAAAA AAGAT GTG TTAGGGT CTC TTTA AAT GTG GACT TTGTG	1669
Db	481	TAA AAAAAA AAGAT GTG TTAGGGT CTC TTTA AAT GTG GACT TTGTG	540
OY	1670	TGTTGTTATGATAAATTAAATATTATTAAGCTGT	1715
Db	541	TGTTGTTATGATAAATTAAATATTATTAAGCTGT	586

Search completed: September 30, 2004, 22:12:45
Job time : 640.881 secs

OM nucleic - nucleic search, using sw model
Run on: September 30, 2004, 21:45:48 ; Search time 138 258 Second
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ALIGNMENT:

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Qy .141 TACTAAATAAATAAAAAAATTAGCTGGAGTGTGTTGGACCCGTAACTCTAGCTA 1500
 Db 1441 TACTAAATAAATAAAAAAATTAGCTGGAGTGTGTTGGACCCGTAACTCTAGCTA 1500
 Qy 1501 CTGGGAGGCCTAACAGGAGAATCTTGACCTTGAGCTGGAGCAGGGTGCAGTGACCG 1560
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 Qy 1561 AGATCTGCCATTGACTCCACCCGGCAACAGAGTGAACTTCCTGAACTTGAGGGAG 1620
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 Qy 1621 AAAAAGAGTTGTATGGCTTCTTTAAATGTGAACTTTTGTTAGTGTTGTTA 1680
 Db 1621 AAAAAGAGTTGTATGGCTTCTTTAAATGTGAACTTTTGTTGTTA 1680
 Qy 1681 TGATCAAATTAAATATTATTTATGACTGTGAGCAAAAAAAAAAAAAGGG 1740
 Db 1681 TGATCAAATTAAATATTATTTATGACTGTGAGCAAAAAAAAAAAAAGGG 1740
 Qy 1741 CGG 1743
 Db 1741 CGG 1743

RESULT 3

US-03-345-882-1/c

; Sequence 1, Application US/09345882

; Patent No. 6399373

; GENERAL INFORMATION:

; APPLICANT: Bougueleret, Yvadie

; TITLE OF INVENTION: A NUCLEAR ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID).

; FILE REFERENCE: GENSET_031A

; CURRENT APPLICATION NUMBER: US/09/345, 882

; CURRENT FILING DATE: 1999-06-30

; PRIOR APPLICATION NUMBER: US 60/091, 315

; PRIOR FILING DATE: 1998-06-30

; PRIOR APPLICATION NUMBER: US 60/111, 909

; PRIOR FILING DATE: 1998-12-10

; NUMBER OF SEQ ID NOS: 140

; SOFTWARE: Patent.pml

; SEQ ID NO 1

; LENGTH: 162450

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: allele

; LOCATION: 72794

; OTHER INFORMATION: 5-124-273 : polymorphic base A or G

; FEATURE:

; NAME/KEY: allele

; LOCATION: 88073

; OTHER INFORMATION: 5-127-261 : polymorphic base A or C

; FEATURE:

; NAME/KEY: allele

; LOCATION: 93714

; OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT

; FEATURE:

; NAME/KEY: allele

; LOCATION: 97122

; OTHER INFORMATION: 99-1442-224 : polymorphic base G or T

; FEATURE:

; NAME/KEY: allele

; LOCATION: 97152

; OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T

; FEATURE:

; NAME/KEY: allele

LOCATION: 99098
 OTHER INFORMATION: 5-130-257 : polymorphic base A or G
 FEATURE:
 NAME/KEY: allele
 LOCATION: 10806
 OTHER INFORMATION: 5-131-395 : polymorphic base A or T
 FEATURE:
 NAME/KEY: allele
 LOCATION: 106540
 OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
 FEATURE:
 NAME/KEY: allele
 LOCATION: 108149
 OTHER INFORMATION: 5-135-198 : polymorphic base insertion of A
 FEATURE:
 NAME/KEY: allele
 LOCATION: 108106
 OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
 FEATURE:
 NAME/KEY: allele
 LOCATION: 108308
 OTHER INFORMATION: 5-135-357 : polymorphic base A or G
 FEATURE:
 NAME/KEY: allele
 LOCATION: 108471
 OTHER INFORMATION: 5-136-174 : polymorphic base C or T
 FEATURE:
 NAME/KEY: allele
 LOCATION: 134362
 OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A
 FEATURE:
 NAME/KEY: allele
 LOCATION: 134374
 OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
 FEATURE:
 NAME/KEY: allele
 LOCATION: 146228
 OTHER INFORMATION: 5-143-84 : polymorphic base A or G
 FEATURE:
 NAME/KEY: allele
 LOCATION: 150329
 OTHER INFORMATION: 5-145-24 : polymorphic base A or G
 FEATURE:
 NAME/KEY: allele
 LOCATION: 160031
 OTHER INFORMATION: 5-148-352 : polymorphic base G or T
 FEATURE:
 NAME/KEY: allele
 LOCATION: 7271..72817
 OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
 FEATURE:
 NAME/KEY: allele
 LOCATION: 88050..88096
 OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID31
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 NAME/KEY: allele
 LOCATION: 88050..88096
 OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
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 NAME/KEY: allele
 LOCATION: 90819..90865
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 FEATURE:
 NAME/KEY: allele
 LOCATION: 93590..93736
 OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
 FEATURE:
 NAME/KEY: allele
 LOCATION: 97059..97145
 OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
 FEATURE:
 NAME/KEY: allele
 LOCATION: 97130..97177
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 NAME/KEY: allele
 LOCATION: 97130..97177
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 LOCATION: 97130..97177
 OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
 FEATURE:
 NAME/KEY: allele
 LOCATION: 99075..99121
 OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID35
 FEATURE:
 NAME/KEY: allele
 LOCATION: 99094..99140
 OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
 FEATURE:
 NAME/KEY: allele
 LOCATION: 103783..103828
 OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
 FEATURE:
 NAME/KEY: allele
 LOCATION: 10618..106966
 OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
 FEATURE:
 NAME/KEY: allele
 LOCATION: 108084..108130
 OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
 FEATURE:
 NAME/KEY: allele
 LOCATION: 108084..108130
 OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59

FEATURE:
 NAME/KEY: allele
 LOCATION: 108127..108177
 OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39

FEATURE:
 NAME/KEY: allele
 LOCATION: 108127..108177
 OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60

FEATURE:
 Query Match 3.3%; Score 58; DB 4; Length 162450;
 Best Local Similarity 100.0%; Pred. No. 7.3e-14; Mismatches 0; Indels 0; Gaps 0;
 Matches 58; Conservative

Qy 1527 CTGAACTGGAGGCAGGGTTCAGTGAGCCAGATCGTGCATGCAACC 1584
 Db 8387 CTGAACTGGAGGCAGGGTTCAGTGAGCCAGATCGTGCATGCAACC 8330

RESULT 4
 US-09-482-273-79
 ; Sequence 79, Application US/09482273
 ; GENERAL INFORMATION:
 ; PATENT NO. 6514631
 ; TITLE OF INVENTION: 71 Human Secreted Proteins
 ; FILE REFERENCE: P2301
 ; CURRENT APPLICATION NUMBER: US/09/482,273
 ; CURRENT FILING DATE: 2000-01-13
 ; EARLIER APPLICATION NUMBER: PCT/US99/15849
 ; EARLIER FILING DATE: 1999-07-14
 ; EARLIER APPLICATION NUMBER: 60/092,921
 ; EARLIER FILING DATE: 1998-07-15
 ; EARLIER APPLICATION NUMBER: 60/092,922
 ; EARLIER FILING DATE: 1998-07-15
 ; EARLIER APPLICATION NUMBER: 60/092,956
 ; EARLIER FILING DATE: 1998-07-15
 ; NUMBER OF SEQ ID NOS: 267
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 79
 ; LENGTH: 2191
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (1327)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (1334)
 ; OTHER INFORMATION: n equals a,t,g, or c

RESULT 5
 US-09-482-273-79
 ; Query Match 2.9%; Score 50; DB 4; Length 2191;
 ; Best Local Similarity 100.0%; Pred. No. 1.5e-10; Mismatches 0; Indels 0; Gaps 0;
 ; Matches 50; Conservative

Qy 1361 TTGGGGAGCTGAGGTGGTGGATCACCTGAGGTGGATCAGGAGTTGAGACCA 1410
 Db 1929 TTGGGGAGCTGAGGTGGTGGATCACCTGAGGTGGATCAGGAGTTGAGACCA 1978

RESULT 6
 US-09-820-924-3
 ; Sequence 3, Application US/09820924
 ; GENERAL INFORMATION:
 ; PATENT NO. 655351
 ; APPLICANT: BEASLEY, Ellen M. et al
 ; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES THEREOF
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: C100123
 ; CURRENT APPLICATION NUMBER: US/09/820,924
 ; CURRENT FILING DATE: 2001-03-30
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 39982
 ; TYPE: DNA
 ; ORGANISM: Human

RESULT 5
 US-09-564-805-2B/C
 ; GENERAL INFORMATION:
 ; Sequence 28, Application US/09564805
 ; PATENT NO. 6313403
 ; APPLICANT: Tsvetkian, Sean V.
 ; APPLICANT: Teng, David H.P.
 ; APPLICANT: Simard, Jacques
 ; APPLICANT: Rommens, Johanna M.
 ; APPLICANT: Myriad Genetics, Inc.
 ; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

Query Match 2.9%; Score 50; DB 4; Length 39982;
 Best Local Similarity 100.0%; Pred. No. 1.1e-10; Mismatches 0; Indels 0; Gaps 0;
 Matches 50; Conservative

RESULT 7 US-09-369-247-46

; Sequence 46, Application US/09369247

; Patent No. 656992

; GENERAL INFORMATION:

; APPLICANT: Robert et al.

; TITLE OF INVENTION: 44 Human Secreted Proteins

; FILE REFERENCE: PZ024P1

CURRENT APPLICATION NUMBER: US/09/369,247

CURRENT FILING DATE: 1999-08-05

EARLIER APPLICATION NUMBER: 60/074,118

EARLIER FILING DATE: 1998-02-09

EARLIER APPLICATION NUMBER: 60/074,157

EARLIER FILING DATE: 1998-02-09

EARLIER APPLICATION NUMBER: 60/074,137

EARLIER FILING DATE: 1998-02-09

EARLIER APPLICATION NUMBER: 60/074,341

EARLIER FILING DATE: 1998-02-09

EARLIER APPLICATION NUMBER: 60/074,141

EARLIER FILING DATE: 1998-02-09

NUMBER OF SEQ ID NOS: 172

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 46

LENGTH: 2094

TYPE: DNA

ORGANISM: Homo sapiens

RESULT 8 US-09-369-247-46

; Sequence 46, Application US/09369247

; Patent No. 656992

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/369,247

CURRENT FILING DATE: 1999-08-05

EARLIER APPLICATION NUMBER: 60/074,118

EARLIER FILING DATE: 1998-02-09

EARLIER APPLICATION NUMBER: 60/074,157

EARLIER FILING DATE: 1998-02-09

EARLIER APPLICATION NUMBER: 60/074,137

EARLIER FILING DATE: 1998-02-09

EARLIER APPLICATION NUMBER: 60/074,341

EARLIER FILING DATE: 1998-02-09

EARLIER APPLICATION NUMBER: 60/074,141

EARLIER FILING DATE: 1998-02-09

NUMBER OF SEQ ID NOS: 172

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 46

LENGTH: 2094

TYPE: DNA

ORGANISM: Homo sapiens

RESULT 9 US-09-369-247-46

; Sequence 46, Application US/09369247

; Patent No. 656992

; GENERAL INFORMATION:

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent. pm

SEQ ID NO 15040

LENGTH: 431

TYPE: DNA

ORGANISM: Homo sapiens

RESULT 10 US-09-435-739-42/C

; Sequence 42, Application US/09435739

; Patent No. 6654105

; GENERAL INFORMATION:

; APPLICANT: Pecker, Iris

; APPLICANT: Vladavsky, Israel

; APPLICANT: Feinstein, Elena

; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE

; FILE REFERENCE: 00/20454

CURRENT APPLICATION NUMBER: US/09/435,739

CURRENT FILING DATE: 2001-06-05

NUMBER OF SEQ ID NOS: 47

SOFTWARE: PatentIn version 3.0

SEQ ID NO 42

LENGTH: 44848

TYPE: DNA

ORGANISM: Homo sapiens

RESULT 11 US-09-435-739-42

; Sequence 42, Application US/09435739

; Patent No. 6654105

; GENERAL INFORMATION:

; APPLICANT: Huang, Tim

; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION

; FILE REFERENCE: UMO1523

CURRENT APPLICATION NUMBER: US/09/497,855A

CURRENT FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: 60/120,592

PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: 60/118,760

PRIOR FILING DATE: 1999-02-05

NUMBER OF SEQ ID NOS: 54

; SOFTWARE: PatentIn version 3.0
; SEQ_ID NO: 38
; LENGTH: 128779
; TYPE: DNA
; ORGANISM: Homo sapiens;
; US-08-451-778A-38

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Best Local Similarity 100.0%; Pred. No. 1.4e-09; Mismatches 0; Indels 0; Gaps 0;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1520 AGATCTCTGGACCTGGAGGAGGTGCACTGAGCGAGATCC 1566
Db 94386 AGATCTCTGGACCTGGAGGAGGTGCACTGAGCGAGATCG 94340

RESULT 12
US-08-451-778A-7/c
Sequence 7, Application US/08451777A
Patent No. 5799223
GENERAL INFORMATION:
APPLICANT: Bergsma, Derk J.
APPLICANT: Stambolian, Dwight J.
TITLE OF INVENTION: Human Galactokinase Gene
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: 709 Swedeland Road/UW2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0319

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,778A
FILING DATE: 26-MAY-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10825
FILING DATE: 23-SEP-1994

ATTORNEY/AGENT INFORMATION:
NAME: Eagle, Alissa M.

REGISTRATION NUMBER: 37,126
REFERENCE/DOCKET NUMBER: P50268-1B

TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5364
TELEFAX: 610-270-5090

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 7676 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-451-778A-7

Query Match 2.6%; Score 45; DB 2; Length 7676;
Best Local Similarity 100.0%; Pred. No. 1.2e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1527 CTGAACTGGGGAGGAGGTGCACTGAGCGAGATCGGCCA 1571
Db 4083 CTGAACTGGGGAGGAGGTGCACTGAGCGAGATCGGCCA 4039

RESULT 14
US-08-998-208-7/c
Sequence 7, Application US/08998208
Patent No. 5880105
GENERAL INFORMATION:
APPLICANT: Bergsma, Derk J.
APPLICANT: Stambolian, Dwight J.
TITLE OF INVENTION: Human Galactokinase Gene
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: 709 Swedeland Road/UW2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0319

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

RESULT 13
US-08-451-778A-7/c
Sequence 7, Application US/08451778A

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,208
FILING DATE: 21-SEP-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/451,777
FILING DATE: 26-MAY-1995
APPLICATION NUMBER: PCT/US94/10825
ATTORNEY/AGENT INFORMATION:
NAME: Eagle, Alissa M.
REGISTRATION NUMBER: 37-126
REFERENCE/DOCKET NUMBER: P50268-1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5900
TELEFAX: 610-270-5364
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 7676 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-998-208-7

RESULT 15
PCT-US95-06743-7/C

Sequence 7, Application PC/TU9506743
GENERAL INFORMATION:
APPLICANT: Bergman, Derk J.
TITLE OF INVENTION: Human Galactokinase Gene
NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESS: 709 Swedeland Road/UM2220
STREET: King of Prussia
CITY: Pennsylvania
STATE: USA
COUNTRY: USA
ZIP: 19406-939

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06743
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10825
FILING DATE: 21-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34-028
REFERENCE/DOCKET NUMBER: P50268-1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 7676 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

Query Match 2.6%; Score 45; DB 5; Length 7676;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1527 CTGAACTTGGAGGAGGTGCACTGAGCCGAGATCGTGCCA 1571
D0 4033 CTGAACTTGGAGGAGGTGCACTGAGCCGAGATCGTGCCA 4039

Search completed: October 1, 2004, 03:56:15
Job time : 141.258 secs

OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 21:52:37 ; Search time 817,411 Seconds
 (without alignments)
 10810.058 Million cell updates/sec

Title: US-10-077-698-2
 perfect score: 1743
 Sequence: tccggactagtcttagacgg.....aaaaaaaaaaaaaggcg 1743

Scoring table: OLIGO_NUC
 Gapop 60.0 , Gapext 60.0

Searched: 3340653 seqs, 2534783154 residues

Word size : 0

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:*

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18: /cgn2_6_ptodata/1/pubpna/US0E_PUBCOMB.seq:*

19: /cgn2_6_ptodata/1/pubpna/US0F_PUBCOMB.seq:*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1743	100.0	1743	Sequence 1, Appli
2	1743	100.0	1743	Sequence 2, Appli
3	1743	100.0	1743	Sequence 3, Appli
4	1743	100.0	1743	Sequence 4, Appli
5	1086	62.3	1086	Sequence 5, Appli
6	1086	62.3	1086	Sequence 6, Appli
7	1086	62.3	1086	Sequence 7, Appli
8	1086	59.4	1086	Sequence 8, Appli
9	1035	59.4	1086	Sequence 9, Appli
10	1035	59.4	1086	Sequence 10, Appli
11	1035	59.4	1086	Sequence 11, Appli
12	984	56.5	1086	Sequence 12, Appli
13	926	53.1	1086	Sequence 13, Appli
14	926	53.1	1086	Sequence 14, Appli

RESULT 1

US-10-086-181-1
 Sequence 1, Application US/10086181
 Publication No. US20020177151A1
 GENERAL INFORMATION:
 APPLICANT: GIMENO, Ruth
 TITLE OF INVENTION: METHODS FOR THE TREATMENT OF DISORDERS, INCLUDING OBESITY
 TITLE OF INVENTION: DISORDERS, INCLUDING OBESITY
 FILE REFERENCE: WO-02-027632
 CURRENT APPLICATION NUMBER: US/10/086,181
 CURRENT FILING DATE: 2002-02-26
 PRIOR APPLICATION NUMBER: 60/271,655
 PRIORITY FILING DATE: 2001-02-26
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 1743
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE: CDS
 NAME/KEY: CDS
 LOCATION: (44)...(1129)

Query Match

Best Local Similarity 100.0%; Pred. No. 0; Matches 1743; Conservative 0; Mismatches 0

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 Db 1 TOCGGACTAGTCTAGACCGCGAGGGCCAGGCG
 Db 1 TOCGGACTAGTCTAGACCGCGAGGGCCAGGCG

Qy 61 GCGGGCACGGCGACGCCCTGCGAGCTGGAGG
 Db 61 GGGGCAAGCGCGACGCCCTGCGAGGCG
 Db 61 CTCTCTCCGACGTCAGGGGACACCCGGCTGGTGC

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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Db	181	GCTGGTGCATCTTGCAGTCGTCCTGCTGGGCAAGGTGGCCTGGCTGGC 240	Qy
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Db	241	GCGCGGACACGGGGGGGGGACTGCCTGGCTGGACTAACCTTCGGGGAACCT 300	Qy
Db	241	GCGCGGACACGGGGGGGGGACTGCCTGGCTGGACTAACCTTCGGGGAACCT 300	Qy
Db	301	GCTTTCATCAGGCTATCCTCTGGCTGGACTGAGGCTGAGGCTGCTGCT 360	Qy
Db	301	GCTTTCATCAGGCTATCCTCTGGCTGGACTGAGGCTGAGGCTGCTGCT 360	Qy
Db	361	GGGGCCCGTGCCTGCCAACCTGCTCTAAGTGATGACCTGAGGGCACGGTC 420	Qy
Db	361	GGGGCCCGTGCCTGCCAACCTGCTCTAAGTGATGACCTGAGGGCACGGTC 420	Qy
Db	421	CCCTACGCGCCGGTCAAGCGGAGCAGCGGACATGGTGTGGGGCTGCTCC 480	Qy
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Db	481	CGTGGCGGAGCTCTGGCGGCGGGCGGGAGTGTGCTGGCTGGCGCTATC 540	Qy
Db	541	GGCGGTGGGGCTCTGGCTCTGGGCTCTGGGCTCTGGGCTCTGGGCTCTGG 600	Qy
Db	541	GGCGGTGGGGCTCTGGCTCTGGGCTCTGGGCTCTGGGCTCTGGGCTCTGG 600	Qy
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Db	661	GTCGGATGCTCTTGATCTTGACTTGACTCTTGCTGGCCAGGACTGTCACTGTGTCAG 720	Qy
Db	721	TTACTCCAATTTAACAGATCACAGAGGATCAAGGAGAGGCTACGGTAGCTGG 780	Qy
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Db	781	CTACTCGGAGGCCACAGATCCGGGTGTCAGCGGACTTCGGCTCTGGCTGG 780	Qy
Db	781	CTACTCGGAGGCCACAGATCCGGGTGTCAGCGGACTTCGGCTCTGGCTGG 780	Qy
Db	840	CTACTCGGAGGCCACAGATCCGGGTGTCAGCGGACTTCGGCTCTGGCTGG 840	Qy
Db	841	CTTCCTCCATGGTCTCTCTCATCATCTGTGAGGCCATCACATCACATCTCT 900	Qy
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Db	900	CATCTGATCCAGAACCTCAAGCAAGAACCTGGCTCTGGCGCTCTCTCTGGGT 960	Qy
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		; Sequence 2, Application US/10077698	
		; Publication No. US20030008350A1	
		; GENERAL INFORMATION:	
		; APPLICANT: Glucksmann, Maria A.	
		; TITLE OF INVENTION: 14213 Receptor, A No. US20030008350a1 G-Protein Coupled	
		; FILE REFERENCE: 5800-4B, 03500/177086	
		; CURRENT APPLICATION NUMBER: US/10/077, 598	
		; CURRENT FILING DATE: 2002-02-13	
		; PRIOR APPLICATION NUMBER: 09/261, 599	
		; PRIOR FILING DATE: 1999-02-26	
		; PRIOR APPLICATION NUMBER: 09/107, 761	
		; PRIOR FILING DATE: 1998-06-30	
		; PRIOR APPLICATION NUMBER: 09/223, 538	
		; PRIOR FILING DATE: 1998-12-30	
		; NUMBER OF SEQ ID NOS: 7	
		; SOFTWARE: PatentIn Ver. 2.1	
		; SEQ ID NO 2	
		; LENGTH: 1743	
		; TYPE: DNA	
		; ORGANISM: Homo sapiens	
		; US-10-077-698-2	
		Query Match 100.0%; Score 1743; DB 15; Length 1743;	
		Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;	
		Matches 1743; Conservative 0;	

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Db	61	GCGGGCAGGGGAGAAGGCCCTTGCGAACCTTAAAGGAACCCGACCCGTTTC	120	Db
QY	121	CTCTCTCGGAGCTCAAGGGCAGCACCGCGACTGGCTGCCCCTGAGGAGCC	180	Db
Db	121	CTCTCTCGGAGCTCAAGGGCAGCACCGCGACTGGCTGCCCCTGAGGAGCC	180	Db
QY	181	GTGGGCTCACTTTCGAGTGTGCTCTGGCAACCTGTCGCCCCCTGCTGTC	240	Db
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QY	301	GTCTCATCAGGGCAACCCGCGCTGAGCTGCCTGCGTGTGACTCAACCTT	300	Db
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QY	241	GGCCGAGACGCCGCGAGCGACTGCCTGCGTGTGACTCAACCTT	360	Db
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QY	541	GCGGGTGGCGCTCTGCTCTCTGGCTCTGAGCTGAGGGCATGTGAGGGCTTC	600	Db
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QY	661	GTGGGATCTCTTGTACTTGACTTCTGGGCCAGGACTGGCATGTGATG	720	Db
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QY	721	TRACTCAAATTTCAGATCAAAAGCATCAGGAGGCTTACGGTAAGCTGG	780	Db
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QY	781	CTACTCTGGAGGCCACCGATCGGCGTCCCGAGACTTCGGCTCTGGACCT	840	Db
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QY	901	CATCTCTCATCCAGAACCTCAAGAACCTGGCTCTCTCTCATGAGCTG	960	Db
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QY	1021	CAGGAAATGAGGAAATTTCGCTCTGGTCCAGAAGAGGCCATT	1080	Db
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Db	1081	AACAGACACATCTGTCAGAGAMATGACTTGTGATTAATTCGCTGTAATT	1140	Db
QY	1141	ACCGCGATTTCTCACCTGGCGACTGTCGACGCTTAAACGAGTCAATT	1200	Db
Db	1141	ACCGCGATTTCTCACCTGGCGACTGTCGACGCTTAAACGAGTCAATT	1200	Db
QY	1201	ACCCCTCATGTCGACCTCTTAAAGAAATGACCTATGCAATAGATCCAGC	1260	Db
Db	1201	ACCCCTCATGTCGACCTCTTAAAGAAATGACCTATGCAATAGATCCAGC	1260	Db
QY	1261	GTGCGCAAGGCTGAGCTGCTCTTAAAGAAATGACCTATGCAATAGATCCAGC	1320	Db
Db	1261	GTGCGCAAGGCTGAGCTGCTCTTAAAGAAATGACCTATGCAATAGATCCAGC	1320	Db
QY	1321	GTGCGCAAGGCTGAGCTGCTCTTAAAGAAATGACCTATGCAATAGATCCAGC	1380	Db
Db	1321	GTGCGCAAGGCTGAGCTGCTCTTAAAGAAATGACCTATGCAATAGATCCAGC	1380	Db
QY	1381	GTGCGCAAGGCTGAGCTGCTCTTAAAGAAATGACCTATGCAATAGATCCAGC	1440	Db
Db	1381	GTGCGCAAGGCTGAGCTGCTCTTAAAGAAATGACCTATGCAATAGATCCAGC	1440	Db
QY	1441	TACTAAAAATAAAAAAAATTACTGGAGTGTGAGCTGAGCTGAGCTGAGGTT	1500	Db
Db	1441	TACTAAAAATAAAAAAAATTACTGGAGTGTGAGCTGAGCTGAGGTT	1500	Db
QY	1501	CTTGGGAGGGTCACTGAGGACTTCGAGACCAACTGAGAACCTGGAGGTTGGAGGTTGGG	1560	Db
Db	1501	CTTGGGAGGGTCACTGAGGACTTCGAGACCAACTGAGAACCTGGAGGTTGGG	1560	Db
QY	1561	AGATGTTGCGATGACTGAGGACCTGGAGGACCACTGGAGGTTGGAGGTTGGG	1620	Db
Db	1561	AGATGTTGCGATGACTGAGGACCTGGAGGTTGGAGGTTGGG	1620	Db
QY	1621	AAAAGAATGTTGCTTAAATGTCGACTGAGCTGAGGTTGGAGGTTGGG	1680	Db
Db	1621	AAAAGAATGTTGCTTAAATGTCGACTGAGGTTGGAGGTTGGG	1680	Db
QY	1681	TGATCAATTATAAAATATTATGACTGTTGAGAACAGGGTCAAGAA	1740	Db
Db	1681	TGATCAATTATAAAATATTATGACTGTTGAGAACAGGGTCAAGAA	1740	Db
QY	1741	CGG 1743	1741	Db
Db	1741	CGG 1743	1741	Db
QY	US-10-015-498-1	RESULT 5		
		; Sequence 1, Application US/10015498		
		; Publication No. US20020151705A1		
		; GENERAL INFORMATION:		
		: APPLICANT: Smith, Kelli B.		
		: TITLE OF INVENTION: DNA Encoding Orphan SNORF49 Receptor		
		: FILE REFERENCE: 601:4		
		: CURRENT APPLICATION NUMBER: US/10/015,498		
		: CURRENT FILING DATE: 2001-12-11		
		: PRIOR APPLICATION NUMBER: US/09/412,933		
		: PRIOR FILING DATE: 1999-10-05		
		: NUMBER OF SEQ ID NOS: 2		
		: SOFTWARE: Patentin Ver. 2.0 - beta		
		: SEQ ID NO: 1		
		: LENGTH: 1160		
		: TYPE: DNA		
		: ORGANISM: Homo sapiens		
		US-10-015-498-1		
Query Match		Best Local Similarity 99.9%; Pred: No. 0; Mismatches 1; Indels 0; Gaps 0;		
Matches 1159; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	17	ACCGCTGGGGCCGCCAGGGGGAACTGGCTCTCTGAGTGGGGGGAGCGGGGAC	76	Db
Db	1	ACCCCTGGGGCCGCCAGGGGGAACTGGCTCTCTGAGTGGGGGGAGCGGGGAC	76	Db

OY	77	GCGCCCTGGCAGCTGGAGCAACGCAACGCCAACCGCTTCCCTTCCTTCAGACGCTC	136
Db	61	GCGCCCTTGCGCACGCAACGCCAACCGCTTCCCTTCCTTCAGACGCTC	120
OY	137	AAGGGGACCCACGGGTGGCTCTGGGGGGAGAACCGTGTGGTGTGTCATCTT	196
Db	121	AAGGGGACCCACGGGTGGCTCTGGGGGGAGAACCGTGTGGTGTGTCATCTT	180
OY	197	GCAGGTGTCGCMGTCGGCAACGTTGGGGGGCTGGTGTGGGGGGAGACAGCTGCG	256
Db	181	GCAGGTGTCGCMGTCGGCAACGTTGGGGGGCTGGTGTGGGGGGAGACAGCTGCG	240
OY	257	GGGGGACTGCGCTGCTGGTACTCAACCTCTCTGGGGGACCTGCTTCATAGGCT	316
Db	241	GGGGGACTGCGCTGCTGGTACTCAACCTCTCTGGGGGACCTGCTTCATAGGCT	300
OY	317	ATCCCCTGGCTCTGGCTGGCTGGCTGACTGGGGCTGGCTGGGGGGCTGGCT	376
Db	301	ATCCCCTGGCTCTGGCTGGCTGGCTGGCTGACTGGGGCTGGCTGGGGGGCTGGCT	360
OY	377	CACCTGCTCTCTAGTGTGATGACCTCTGGCTGGCTGACTGGGGCTGGCTGGCT	436
Db	361	CACCTGCTCTCTAGTGTGATGACCTCTGGCTGGCTGACTGGGGCTGGCTGGCT	420
OY	437	GTCACCTGCGCTCTGGCTGGCTGACTGGGGCTCATCTGGGGGAGCTCTCTGG	496
Db	421	GTCACCTGCGCTGACTGGGGCTCATCTGGGGGAGCTCTCTGGGGGAGCTCTGG	480
OY	497	CGGGGGCGGGGGCTGCTGGGCTCATCTGGGGTATCTGGGGCTGGGGCTGGCT	556
Db	481	CGGGGGCGGGGGCTGCTGGGCTCATCTGGGGTATCTGGGGCTGGGGCTGGCT	540
OY	557	CCTCTCTGCGCTCTTCGAGTCGTCGCCACGGCTCCGGGGGCGACCGGAATT	616
Db	541	CCTCTCTGCGCTCTTCGAGTCGTCGCCACGGCTCCGGGGGCGACCGGAATT	600
OY	617	TGAGTTGCAACTCTTTGGCCACCATCTCTGGAGAGATCTGGGGATGTCCTTT	676
Db	601	TGAGTTGCAACTGATTGGCCACCATCTCTGGAGAGATCTGGGGATGTCCTTT	660
OY	677	GTACTTGTAACTCTTGCTGGCCAGACTGCTGCTGCGGAAACTGTCCTGGGAAATT	736
Db	661	GTACTTGTAACTCTTGCTGGCCAGACTGCTGCTGCGGAAACTGTCCTGGGAAATT	720
OY	737	CAGATCACAAAGGCACTCAGGGAGAGCTACCGTAACGCTTGGGACTCGAGGCCAC	796
Db	721	CAGATCACAAAGGCACTCAGGGAGAGCTACCGTAACGCTTGGGACTCGAGGCCAC	780
OY	797	CAGATCACAAAGGCACTCAGGGAGAGCTACCGTAACGCTTGGGACTCGAGGCCAC	856
Db	781	CAGATCACAAAGGCACTCAGGGAGAGCTACCGTAACGCTTGGGACTCGAGGCCAC	840
OY	857	TCCTCTCTCATCTGAGGCCCATCATCACCACTCATCCCTCATCTGATCGAGAC	916
Db	841	TCCTCTCTCATCTGAGGCCCATCATCACCACTCATCCCTCATCTGATCGAGAC	900
OY	917	TTCAAGCAAGCTGGCATCTGGCGCCCTCTCTCTGAGGGGGCTTCACATT	976
Db	901	TTCAAGCAAGCTGGCATCTGGCGCCCTCTCTGAGGGGGCTTCACATT	960
OY	1037	AAATTTTGTGCTGCTGCTGAGGAGGAGCATTTAACAGACACTCTGTC	104
Db	1021	AAATTTTGTGCTGCTGAGGAGCATTTAACAGACACTCTGTC	100
OY	1097	AAAAGAATGACTTGTGATATTCTGGATAATTCTTAAAGCCGAGTTCTCACA	115
Db	1081	AAAAGAATGACTTGTGATATTCTGGATAATTCTTAAAGCCGAGTTCTCACA	114

RESULT 6
US-10-086-181-3
; Sequence 3, Application US/10086181
; Publication No. US20020177151A1
; GENERAL INFORMATION:
; APPLICANT: GIMENO, Ruth
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF METABOLIC
; DISORDERS, INCLUDING OBESITY AND DIABETES
; FILE REFERENCE: MNI-220
; CURRENT APPLICATION NUMBER: US/10/086,181
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 60/271,655
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FasSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1086
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-086-181-3

QY 704 CTGGCATGTTGATGACTTCAAAATTAGCAGATCACAAGGATCAAGGAGG 763
Db 661 CTGGCATGTTGATGACTTCAAAATTAGCAGATCACAAGGATCAAGGAGG 720
QY 754 CTACGGTAAGCTGGCTACTCGAGGCCAGGAGCTGGAGCTGGAAAGCC 823
Db 721 CTACGGTAAGCTGGCTACTCGAGGCCAGGAGCTGGAGCTGGAGACTTC 780
QY 824 CGGCCTCGCACCTCTCCCTCATGTCTCTCATATGTGGAGGCCATC 883
Db 781 CGGCCTCGCACCTCTCCCTCATATGTGGAGGCCATC 840
QY 884 ATCATCACCATCTCTCATCTCATCGAGGCCAGGAGCTGGAGCCATC 943
Db 841 ATCATCACCATCTCTCATCTCATCGAGACTCGAGAGCTGGGG 900
QY 944 TCCCTCTCTCTGGTGGCTCATCTGTTCAATGCCCTAACCCCATCC 1003
Db 901 TCCCTCTCTCTGGTGGCTCATCTGTTCAATGCCCTAACCCCATCC 960
QY 1004 TACACATGACACTTGCGAGAATGCTGAGAATTTTGCTGCTCTGGTCCC 1063
Db 951 TACACATGACACTTGCGAGAATTTTGCTGCTCTGGTCCC 1020
QY 1064 GAAAGGGGCCATTAAAGACACATCTGTCAGAAGAATGACTTGCTGATTTCT 1123
Db 1021 GAAAGGGGCCATTAAACAGACACATCTGTCAGAAGAATGACTTGCTGATTTCT 1080
QY 1124 GGCTAA 1129
Db 1081 GGCTAA 1086

RESULT 7
US-10-083-168-11
: Sequence 11, Application US/10083168
; Publication No. US20030023069A1
; GENERAL INFORMATION:
; APPLICANT: Liaw, Chen W.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; APPLICANT: Maciejewski-Lenior, Dominique
; APPLICANT: Leonard, James N.
; APPLICANT: Ortuno, Daniel
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Endogenous And No. US20030023069A1-Endogenous, Constitutively Act
; CURRENT APPLICATION NUMBER: US/10/083,168
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1086
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-083-168-11

Query Match 62.3%; Score 1086; DB 15; Length 1086;
Best Local Similarity 100.0%; Pred. No: 0;
Matches 1086; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AACCCACCGCTTCCCTCTCCAGCTAGGGGACCAACGGCTGGCTTGCC 163
Db 61 AACGGACCGCTTCCCTCTCCAGGACGACCGCTGGCTGCC 120
Db 1 ATGCCCCCTGAATGCGCGGGACGGGGACGGCCCTGGCGACGCC 60
QY 164 GCGGTGGAGACACGGCTGGCTCATCTTGGAGCTGCGCTGCTGGAGAACGCC 223

QY 224 GCGCTGGCTGGGGCGCGCGAGAGGCCGGGGGACTCTGGTGTACTCAC 283
Db 181 GCGCTGGCTGGGGCGCGCGAGAGGCCGGGGACTCTGGTGTACTCAC 240
QY 284 CTCTCTGGGGACTCTGGTGTACTCGAGGAGCCAGATCGCGGTCCAGGACTTC 343
Db 241 CTCTCTGGGGACTCTGGTGTACTCGAGGAGCCAGATCGCGGTCCAGGACTTC 300
QY 344 ACTAGGGCTGCTGGCTGGGGCTGGCTGGGGACTCTGGTGTACTGGCTGGCTGG 403
Db 301 ACTAGGGCTGCTGGGGACTCTGGTGTACTGGCTGGCTGGCTGGCTGG 360
QY 404 AGGGGAGGGTGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGG 463
Db 361 AGGGGAGGGTGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGG 420
QY 464 GTGACCTGGAGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGG 523
Db 421 GTGACCTGGAGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGG 480
QY 524 CTGACCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGG 583
Db 481 CTGACCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGG 540
QY 584 CGGACGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGG 643
Db 541 CGGACGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGG 600
QY 644 ATTCTGGAGAGATCTGGATGTTGACTTCTGGCTCTGGCTGGGGCTGGGGCTGG 703
Db 601 ATTCTGGAGAGATCTGGATGTTGACTTCTGGCTCTGGGGCTGGGGCTGG 660
QY 704 CTGGCATGTTGATGACTTCAAAATTAGCAGATCACAAGGAGG 763
Db 661 CTGGCATGTTGATGACTTCAAAATTAGCAGATCACAAGGAGG 720
QY 764 CTACGGTAAGCTGGCTACTCGAGGCCAGGAGCTGGGGTCCAGGAGACTTC 823
Db 721 CTACGGTAAGCTGGCTACTCGAGGCCAGGAGCTGGGGTCCAGGAGACTTC 780
QY 824 CGGCCTCGCACCTCTCATCTGTCAGAAGAATTTCTCATCTGGAGGCCATC 883
Db 781 CGGCCTCGCACCTCTCATCTGTCAGAAGAATTTCTCATCTGGAGGCCATC 840
QY 884 ATCATCACCATCTCTCATCTGTCAGAAGAATTTCTCATCTGGAGGCCATC 943
Db 841 ATCATCACCATCTCTCATCTGTCAGAAGAATTTCTCATCTGGAGGCCATC 900
QY 944 TCCCTCTCTCTGGTGGCTCATCTGTTCAATGCCCTAACCCCATCTC 1003
Db 901 TCCCTCTCTCTGGTGGCTCATCTGTTCAATGCCCTAACCCCATCTC 960
QY 1004 TACACATGACACTTGCGAGAATTTTGCTGCTCTGGTCCC 1063
Db 961 TACACATGACACTTGCGAGAATTTTGCTGCTCTGGTCCC 1020
QY 1064 GAAAGGGGCCATTAAAGACACATCTGTCAGAAGAATTTTGCTGCTCTGGTCCC 1123
Db 1021 GAAAGGGGCCATTAAACAGACACATCTGTCAGAAGAATTTTGCTGCTCTGGTCCC 1086

RESULT 8
US-09-932-331-1
: Sequence 1, Application US/09992331
; Publication No. US2003002186A1
; GENERAL INFORMATION:
; APPLICANT: FEDER, JOHN N.

; TITLE OF INVENTION: PITUITARY GLAND AND COLON CARCINOMA CELLS
 ; FILE REFERENCE: DO048 CIR
 ; CURRENT APPLICATION NUMBER: US/10/262,313
 ; CURRENT FILING DATE: 2002-09-30
 ; PRIOR APPLICATION NUMBER: U.S. 09/992,331
 ; PRIOR FILING DATE: 2001-11-14
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: Patentin Version 3.1
 ; SEQ ID NO: 1
 ; LENGTH: 1086
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-262-311-1.
 Query Match 59.4%; Score 1035; DB 15; Length 1086;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1085; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 Qy 44 ATGTCGCCCTGATCGCGGGCTTGAGTCGCTGGGG 103
 Db 1 ATGTCGCCCTGATCGCGGGCTTGAGTCGCTGGGG 60
 Qy 104 AACGGCACCGCTTCCCTTCTCGAAGGCAACGGGTGGCC 223
 Db 61 AACGGCACCGCTTCCCTTCTCGAAGGCAACGGGTGGCC 163
 Qy 224 GCCTTGNGCTGGCGCGCGACGCGCCGGGGACTCTGGTCTCAC 283
 Db 181 GCCTTGNGCTGGCGCGCGACGCGCCGGGGACTCTGGTCTCAC 240
 Qy 284 CTCTCTGGGGACCTGTGCTTCATCGGCTATCCCTGGCTGG 343
 Db 241 CTCTCTGGGGACCTGTGCTTCATCGGCTATCCCTGGCTGG 300
 Qy 344 ACTGAGGCCCTGCCTGCTGCTCATCTTGAGTGTGACCTG 403
 Db 301 ACTGAGGCCCTGCCTGCTGCTCATCTTGAGTGTGACCTG 360
 Qy 404 AGCGAACGGTACATCTCGGGGCTTGAGTCGCTGGGG 523
 Db 594 CGCGAACGGTCCGGGCGGACAGGAATTGAGTTGAGTCGCTGGGG 643
 Qy 524 CTCACTCTGGGTATCTCGGGGCTTGAGTCGCTGGGG 583
 Db 481 CTCACTCTGGGTATCTCGGGGCTTGAGTCGCTGGGG 540
 Qy 644 ATTCCTGGAGAGATCTGGGATGCTTGTACTTGTGAACTTGGTCCAGA 703
 Db 601 ATTCCTGGAGAGATCTGGGATGCTTGTACTTGTGAACTTGGTCCAGA 660
 Qy 704 CTGGTCTGATGTACTACTCAAATTACAGATCACAAAGGCAAGGAGG 763
 Db 661 CTGGTCTGATGTACTACTCAAATTACAGATCACAAAGGCAAGGAGG 720
 Qy 764 CTCAAGGTAAGCTGGCTACTCGAGAACCGACAGATCGGGGTCGGCAAGGACTC 823
 Db 721 CTCAAGGTAAGCTGGCTACTCGAGAACCGACAGATCGGGGTCGGCAAGGACTC 780
 Qy 824 CGCTCTTCCGACACCTCTCCCTCACTGTCCTCTCATGTTGAGGCCCATC 883
 Db 781 ATCATACCATCTCTCATCTCATCCGAGAACCTCAAGGAGACTCTGGGG 943
 Qy 884 ATCATACCATCTCTCATCTCATCCGAGAACCTCAAGGAGACTCTGGGG 940
 Db 841 TTCAACATCCCTCATCTCATCCGAGAACCTCAAGGAGACTCTGGGG 900
 Qy 944 TCCTCTCTCTGGGTGGCTTACATTGCTTAATCAGCCCTAACCCCTACCTC 1003
 Db 901 TCCTCTCTCTGGGTGGCTTACATTGCTTAATCAGCCCTAACCCCTACCTC 960
 Qy 1004 TCAACATGACACTGTGAGGATGACTGAGAAGAAATTTCCTGCTCTGTTCCA 1063
 Db 961 TACAAACATGACACTGTGAGGATGACTGAGAAGAAATTTCCTGCTCTGTTCCA 1020
 Qy 1064 GAAGGGGAGCCATTTCAGAGACATGTGAGAAGAAATTTCCTGCTCTGTTCCA 1123
 Db 1021 GAAAAGGAGCCATTTCAGAGACATGTGAGAAGAAATTTCCTGCTCTGTTCCA 1080
 Qy 1124 GGCTAA 1129
 Db 1081 GGCTAA 1086

Qy 351 CCGGGCTGACCCATTGCTGCACCTCTTACATGATGACCTGAGGGCA 4110

Db 308 CCTGGCTACTGACCCATTGCTGCACCTCTTACATGATGACCTGAGGGCA 367

Qy 411 GCGTACATCTCACCTGGGGGTCACTGGGGGAGGGCA TGGTGCGATGTGACC 470

Db 368 GCGTCACCATCCTCACGTTGGGGGAGGGCA TGGTGCGATGTGACC 427

Qy 471 TCGAGCGCGCTGGGGGTCACTGGGGGAGGGCA TGGTGCGATGTGACC 530

Db 428 TCGAGCGCGCTGGGGGTCACTGGGGGAGGGCA TGGTGCGATGTGACC 487

Qy 531 GGGGCTATTCGGGGTCCGGTCTGGCTCTGGGTTCTGGAGTCGGCCGAC 590

Db 488 GGGCTATTCGGGGTCCGGTCTGGAGTCGGCCGCTATGGGTTCTGGAGTCGGCCGAC 547

Qy 591 GCGAGATCTGGGGATCTCTTGTACTTGAACTCTGAGTCGGTCCAGACTGGGCA 710

Db 548 GCGTCGGGGGAGGGAAATTGCGATGTTGACCTGTTGGCCACATTCCTG 607

Qy 608 GAGAGATCTGGGGATCTCTTGTACTTGAACTCTGAGTCGGTCCAGACTGGCA 650

Db 667 TCTGGTACGTTACTCCAAATTACAGATAAAGGGCATCAAGGAGAGGCTCAGG 770

Qy 668 TCTGGTACGTTACTCCAAATTACAGATAAAGGGCATCAAGGAGAGGCTCAGG 727

Db 771 TACGCTGGCTACTCGAGAGGACCGATCGGGTCTCCAGAGCTTCAGG 830

Db 728 TACGCTGGCTACTCGAGAGGACCGATCGGGTCTCCAGAGCTTCAGG 787

Qy 831 TCGCACCCCTCTCTCTCATGTCCTCTCTCATGTCGAGGCCATCATCA 890

Db 848 CAATCCCTCTCATCTGATCACAGAACCTCAGAGCTTCAGG 907

Qy 788 TCGCACCCCTCTCTCATGTCGAGGCCATCATCA 847

Db 891 CATCCCTCTCATCTGATCACAGAACCTCAGGCTCATCGGGCTCCCT 950

Qy 844 CAATCCCTCTCATCTGATCACAGAACCTCAGG 967

Qy 951 TCTCTGGGGGCTCACATTGTAATCAGCCCTAACCCATCTCTACACA 1010

Db 908 TCTCTGGGTGGCTCACATTGTAATCAGCCCTAACCCATCTCTACACA 967

Qy 1011 TACACTGTGAGGAATGAGTGGAGAAATTGTTGCTCTGGTCTCCAGAAG 1070

Db 968 TACACTGTGAGGAATGAGTGGAGAAATTGTTGCTCTGGTCTCCAGAAG 1027

Qy 1071 GGGCCATTAAAGACATCTGTCAAAAGAAATGACTGTGAGATATTCTGGCTAA 1129

Db 1028 GGGCCATTAAAGACATCTGTCAAAAGAAATGACTGTGAGATATTCTGGCTAA 1086

RESULT 15
US-09-992-331-4; Sequence 4, Application US/0992331
; Publication No. US20030022186A1

; GENERAL INFORMATION:

; APPLICANT: FEDER, JOHN N.

; APPLICANT: MINTIER, GABE S.

; APPLICANT: RAMANATHAN, CHANDRA S.

; APPLICANT: HAWKEN, DONALD R.

; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY18,

; TITLE OF INVENTION: EXPRESSED HIGHLY IN PITUITARY GLAND AND COLON CARCINOMA

; TITLE OF INVENTION: CELLS

; FILE REFERENCE: D0048NP

; CURRENT APPLICATION NUMBER: US/09/992,331

; CURRENT FILING DATE: 2001-11-1

; PRIOR APPLICATION NUMBER: 60/308,540

; PRIOR FILING DATE: 2001-07-27

; PRIOR APPLICATION NUMBER: 60/261,782

; PRIOR FILING DATE: 2001-01-16

; PRIORITY APPLICATION NUMBER: 60/248,483

; PRIORITY FILING DATE: 2000-11-14

; NUMBER OF SEQ ID NOS: 45

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 4

; LENGTH: 632

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-992-331-4

; Query Match Similarity 33.6%; Score 586; DB 10; Length 632;

; Best Local Similarity 100.0%; Pred. No. 3-5e-27; Indels 0; Gaps 0;

; Matches 586; Conservative 0; Mismatches 0;

; Qy 1130 TTTTCTTATAGCCGAGTTCTACACTCTGGGAGCTGTCCTGTCATTTAAACAGT 1189

; Db 61 TCTTCTTATAGCCGAGTTCTACACTCTGGGAGCTGTCATTTAAACAGT 60

; Qy 1250 ACATCCACAGCGTGGPAAATTAGGGGGTGTACCAAGGTTCTAATATTTCCTTA 1309

; Db 121 ACATCCACAGCGTGGPAAATTAGGGGGTGTACCAAGGTTCTAATATTTCCTTA 180

; Qy 1310 TAAAGGTTGTGGCAGGTCAGTGTCTATGCCAGCACTTAAAGAATGACCTATGCAATAG 1369

; Db 181 TAAAGGTTGTGGCAGGTCAGTGTCTATGCCGTAATCCACAGCAGTTGGGG 240

; Qy 1370 CTGAGGTGGTGGATCACTGGGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAG 1429

; Db 241 CTGAGGTGGTGGATCACTGGGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAG 300

; Qy 1430 ACCCCCCTCTCTAAATAAAAAAAATTAGCTGGAGTGGTGGTGGGCCACCTGT 1489

; Db 301 ACCCCCCTCTCTAAATAAAAAAAATTAGCTGGAGTGGTGGTGGGCCACCTGT 360

; Qy 1490 ATCTCTACTCTGGGGGTCAGGAGATCTCTGACCTGGGGAGGGT 1549

; Db 421 GCGTGGCCAGGATCGGCCATTCACCCAGGCAACAGGTCAGGTCAG 480

; Qy 1610 TAAAAAATAAAAAAAAGATTTGTTGGGTTCTTTAAATGTAATGACTTTTAGTG 1669

; Db 481 TAAAAAATAAAAAAAAGATTTGTTGGGTTCTTTAAATGTAATGACTTTAGTG 540

; Qy 1670 TCTTGTATATGATCAAATTATAATTATGTTGACTTTAGTGTT 1715

; Db 541 TGTGTGATATGATCAAATTATAATTATGTTGACTTTAGTGTT 586

; Search completed: October 1, 2004, 04:22:19
; Job time : 823.411 secs

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Score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	% Length	DB ID	Description
1	1560	100.0	1560	6 BD240721	BD240721_14273 rec
2	1560	100.0	1560	6 BD269631	BD269631_14273 rec
3	1560	100.0	1560	6 AR228217	AR228217 Sequence
4	1560	100.0	1560	6 AR372102	AR372102 Sequence
5	947	60.7	1419	10 BC053638	BC053638 Mus muscu
6	744	47.7	1086	10 AT288424	AT288424 Mus muscu
7	5.9	38.2	180944	10 AC112153	AC112153 Mus muscu
8	596	38.2	235978	2 AC101774	AC101774 Mus muscu
9	181	11.6	181	6 AR228218	AR228218 Sequence
10	8.8	138	6 AR228219	AR228219 Sequence	
11	6.5	835	10 BC049237	BC049237 Mus muscu	
12	92	5.9	169206	10 AC123550	AC123550 Mus muscu
13	92	5.9	277603	2 AC079543	AC079543 Mus muscu
14	77	4.9	212822	2 AC080156	AC080156 Rattus no
15	77	4.9	225030	10 AC107608	AC107608 Rattus no
16	77	4.9	247337	2 AC098268	AC098268 Rattus no
17	77	4.9	249741	2 AC096330	AC096330 Rattus no
18	77	4.9	271367	2 AC105467	AC105467 Rattus no
19	77	4.9	277195	2 AC080155	AC080155 Rattus no
20	57	3.7	238070	2 AC134313	AC134313 Rattus no
21	57	3.7	242260	2 AC094567	AC094567 Rattus no
22	57	3.7	255120	2 AC127219	AC127219 Rattus no
23	51	3.3	187746	2 AC087123	AC087123 Mus muscu
24	49	3.1	271995	2 AC080155	AC080155 Rattus no
25	44	2.8	744	9 AY255573	AY255573 Homo sapi
26	44	2.8	1086	6 AX98184	AX98184 Sequence
27	44	2.8	1321	6 AX168141	AX168141 Sequence
28	44	2.8	1743	6 AR372101	AR372101 Sequence
29	44	2.8	1737	6 AX15337	BD015337 Novel pol
30	44	2.8	1743	6 BD240720	BD240720_14273 rec
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32	44	2.8	1743	6 AR228216	AR228216 Sequence
33	44	2.8	1743	6 AX657504	AX657504 Sequence
34	42	2.7	933	6 AX657504	AX657504 Sequence
35	40	2.6	1066	6 AX49396	AX49396 Sequence
36	40	2.6	1104	6 AX330123	AX330123 Sequence
37	40	2.6	1131	9 AY288417	AY288417 Homo sapi
38	40	2.6	163964	9 AL356214	AL356214 Human DNA
39	39	2.5	638	6 AX277776	AX277776 Sequence
40	39	2.5	4291	9 HSMB8767	BX647721 Homo sapi
41	38	2.4	203	9 AF3366582	AF3366582 Homo sapi
42	38	2.4	241	6 BD210582	BD210582 Human gen
43	38	2.4	487	6 AX886416	AX886416 Sequence
44	38	2.4	487	6 BD026026	BD026026 Sequence
45	38	2.4	762	6 BD079639	BD079639 Cancer
ALIGNMENTS					
RESULT 1					
BB240721	BB240721	1560 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	14273 receptor, a G-protein coupled receptor.				
DEFINITION					
ACCESSION	BB240721				
VERSION	BB240721.1				
KEYWORDS	GI:33050491				
SOURCE	unidentified				
ORGANISM	unclassified				
	(bases 1 to 1560)				
REFERENCE	Glucksmann,M.A. and Tsai,F.Y.				
AUTHORS					
TITLE	14273 receptor, a G-protein coupled receptor				
JOURNAL	Patent: JP 2002522011-A 2 23-JUL-2002;				
MILLENNIA PHARMACEUTICALS INC					

Pred. No. is the number of results predicted by chance to have a

COMMENT	OS	Murine ortholog
PN	JP	2002522011-A/2
PD	23-JUL-2002	
PR	30-JUN-1999 JP	2000557364
PR	30-JUN-1998 US	09/26/1999
PI	MARIA ALEXANDRA GLUCKSMANN, FONG YING TSAI	
PC	C12N15/09, C07K14/705, C07K16/28, C12N1/15, C12N1/19, C12N1/21, PC	
PC	C12P21/02, C12Q1/68, G01N3/15, G01N3/50, G01N3/53//C12P21/08,	
PC	C12N5/00	
CC	14273 receptor, a G-protein coupled receptor	
FH	Key	
FT	source	1..1560
FT	location/Qualifiers	/organism='Murine ortholog'.
FEATURES	source	1..1560
ORIGIN		/organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644"
Query Match	Best Local Similarity	100.0%; Score 1560; DB 6; Length 1560;
	Matches	1560; Conservative 0; -Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	TGCGCAAGCTCAGGTAAGCCCTTCACATCGCAATCTCACAGAGGGGTCTCGAGGCC
Db	1	TGCGCAAGCTCAGGTAAGCCCTTCACATCGCAATCTCACAGAGGGGTCTCGAGGCC
Qy	61	TGCGCAAGCTCAGGTAAGCCCTTCACATCGCAATCTCACAGAGGGGTCTCGAGGCC
Db	61	TGCGCAAGCTCAGGTAAGCCCTTCACATCGCAATCTCACAGAGGGGTCTCGAGGCC
Qy	121	TGATGACCTCTTGACACCCACGAGGGCTTGAGCTTGACACCCACGAGGGCTTGAG
Db	121	TGATGACCTCTTGACACCCACGAGGGCTTGAGCTTGACACCCACGAGGGCTTGAG
Qy	181	GCGGGGCGCCCGCATGCCCCCTGAGTGTGACACCCACGAGGGCTTGAGCTTGAG
Db	181	GCGGGGCGCCCGCATGCCCCCTGAGTGTGACACCCACGAGGGCTTGAGCTTGAG
Qy	241	CCTGGACCAAGTCATGCCAACCTCCCTCTCGATGTCAGGCCACCC
Db	241	CCTGGACCAAGTCATGCCAACCTCCCTCTCGATGTCAGGCCACCC
Qy	301	GTTGGTGTGAGGCTCTGGGAGACCGCTCTGGACTCTCATCTTCTGCTCACTCC
Db	301	GTTGGTGTGAGGCTCTGGGAGACCGCTCTGGACTCTCATCTTCTGCTCACTCC
Qy	361	TGGCAACGCTGTTGCTCTAGTCTGGGAGCCGGCGACCGCTGAGCCA
Db	361	TGGCAACGCTGTTGCTCTAGTCTGGGAGCCGGCGACCGCTGAGCCA
Qy	421	GCCTGGTGTCAACCTCTGCCGGATTGCTCTGCCAGGCCATCCCTAGTC
Db	421	GCCTGGTGTCAACCTCTGCCGGATTGCTCTGCCAGGCCATCCCTAGTC
Qy	481	TGGTGTGTGGCTCAACTCTGCCGGATTGCTCTGCCAGGCCATCCCTAGTC
Db	481	TGGTGTGTGGCTCAACTCTGCCGGATTGCTCTGCCAGGCCATCCCTAGTC
Qy	541	ACGTGATGACATGAGCGCGACGCTCACATCTGCGGCGCTGAGCTGGAC
Db	541	ACGTGATGACATGAGCGCGACGCTCACATCTGCGGCGCTGAGCTGGAC
Qy	601	GCATGTGCGCATGTCGCGCTCCGGCGCGCTGAGCGCCCGGGCGACTCAG
Db	601	GCATGTGCGCATGTCGCGCTCCGGCGCGCTGAGCGCCCGGGCGACTCAG
Qy	661	GGGACTGTGCGCTCATATGGGTTACTCTGGCTCCCGCGCTGCGCCCTACATC
Db	661	GGGACTGTGCGCTCATATGGGTTACTCTGGCTCCCGCGCTGCGCCCTACATC
RESULT 2	DB269631	
LOCUS	BD269631	1560 bp DNA linear PAT 17-JUL-2003
DEFINITION	14273 receptor, a novel G-protein coupled receptor.	
ACCESSION	BD269631	
VERSION	BD269631.1	GI:33073399
KEYWORDS	BD269631.2	JP 200253997-A/2.
SOURCE	Mus sp.	
ORGANISM	Mus sp.	
	Bukaryota; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 1560)	
AUTHORS	Gluckmann,M.A. and Tsai,F.Y.	
TITLE	14273 receptor, a novel G-protein coupled receptor	

JOURNAL	Patient: JP 2002536997-A 2 05-NOV-2002;
COMMENT	MILLENNIUM PHARMACEUTICALS INC
OS	Mus sp. (murine)
PN	JP 2002536997-A/2
PD	05-NOV-2002
PP	28-FEB-2000 JP 20000601160
PR	26-FEB-1999 US 09/261599, 08-DEC-1999 US 09/456455 PI
PC	MARIA ALEXANDRA GLUCKSMANN, FONG YING TSAI
PC	C12N15/09, C07K14/7705, C07K16/28, C12N1/15, C12N1/19, C12N1/21, PC
PC	C12N5/10,
PC	C12P21/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, G01N33/566,
PC	C12N5/00,
CC	C12N5/00
FH	Murine ortholog
PH	Location/Qualifiers
PT	Key source 1. 1560 /organism='Mus sp. (murine)'.
FEATURES	source 1. 1560 /organism='Mus sp.' /mol_type="genomic DNA" /db_xref="taxon:10095"
ORIGIN	
Query Match	100.0%; Score 1560; DB 6; Length 1560;
Best Local Similarity	100.0%; Pred. No. 0;
Matches	1560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 TGGCCAAGCTCAGCGTAAGCCCTCCACTCGCACTTCAGAAGGGGTCTAGGAGGC 60
Db	1 TTGCCAAGCTCAGCGTAAGCCCTCCACTCGCACTTCAGAAGGGGTCTAGGAGGC 60
Oy	61 TTACACCATCTAGTGACCACTCCGACTGTCCGGCTTACCGAATCTCACGGAG 120
Db	61 TTACACCATCTAGTGACCACTCCGACTGTCCGGCTTACCGAATCTCACGGAG 120
Oy	121 TCGATGACCTCTGACAGCCACAGGGCGCACTCGGAGCTCGGAGCTCGGAG 180
Db	121 TCGATGACCTCTGACAGCCACAGGGCGCACTCGGAGCTCGGAGCTCGGAG 180
Oy	181 GCGGGGCCCCGATGCCCCCTGAGTGCGAACAGGAGGCCCCGGCTCCGGACA 240
Db	181 GCGGGGCCCCGATGCCCCCTGAGTGCGAACAGGAGGCCCCGGCTCCGGACA 240
Oy	241 CCTGGACCAAGTCATGCCCACTTCTCTCGATGTCAGGGCACACC 300
Db	241 CCTGGACCAAGTCATGCCCACTTCTCTCGATGTCAGGGCACACC 300
Oy	301 GGTGGTTGAGGGCTGGAGGACCGTCTGGAGCTCTGGAGCTCTGGAGCT 360
Db	301 GGTGGTTGAGGGCTGGAGGACCGTCTGGAGCTCTGGAGCTCTGGAGCT 360
Oy	361 TGGCGAAAGTGTGCTCTAGTCTGGAGGCCCCGGCGCGCTGGAGCT 420
Db	361 TGGCGAAAGTGTGCTCTAGTCTGGAGGCCCCGGCGCGCTGGAGCT 420
Oy	421 GCGCTGCTCAACCTCTGGCGGATTGCTCTACCAAGGCCATCCCTAGTC 480
Db	421 GCGCTGCTCAACCTCTGGCGGATTGCTCTACCAAGGCCATCCCTAGTC 480
Oy	481 TCGTGTGGCTGGACTGAGGCCCTGGCTGGCTGGCTGGCTGGCTGGCT 540
Db	481 TCGTGTGGCTGGACTGAGGCCCTGGCTGGCTGGCTGGCTGGCTGGCT 540
Oy	541 AGGTGATGACATGAGCGAGCGCTCACCATCTCACACTGCGCGGGTCACTGGAGC 600
Db	541 AGGTGATGACATGAGCGAGCGCTCACCATCTCACACTGCGCGGGTCACTGGAGC 600
Oy	601 GATGGTGTGACATGTCGCCCCCGCGCGCTGGAGGCCCGGGGGGGGACTCGG 660
Db	601 GATGGTGTGACATGTCGCCCCCGCGCGCTGGAGGCCCGGGGGGGGACTCGG 660
Oy	661 CGGCACTGTCGCTTCATATGGGTTACTCGGGCTCGCCGCTGCCCTACATCT 720
Db	661 CGGCACTGTCGCTTCATATGGGTTACTCGGGCTCGCCGCTGCCCTACATCT 720
Oy	721 TGTTCGGCTGGCCGGAGCGCTCCGGCGGGAGCAGGAATTCGATTGCACT 780
Db	721 TGTTCGGCTGGCCGGAGCGCTCCGGCGGGAGCAGGAATTCGATTGCACT 780
Oy	781 TGGATGGCCCAACCGCTAGGAGAAACTCATGGAGTGTATTGACTTGACAT 840
Db	781 TGGATGGCCCAACCGCTAGGAGAAACTCATGGAGTGTATTGACTTGACAT 840
Oy	841 TCCCTGGCGGACTCTGATGTCAGTACTCAAATTAGATCAGATCGAGAC 900
Db	841 TCCCTGGCGGACTCTGATGTCAGTACTCAAATTAGATCAGATCGAGAC 900
Oy	901 CATCGCGAGAGGCTTAGCTGAGCTGCTGGCTGATCTGAGATCGAGAC 900
Db	901 CATCGCGAGAGGCTTAGCTGAGCTGCTGGCTGATCTGAGATCGAGAC 900
Oy	961 CCCACAGACTACCGAGCTCTGGAGCTCTGGCTCTCATGGTTCTTCATCA 1020
Db	961 CCCACAGACTACCGAGCTCTGGCTCTCATGGTTCTTCATCA 1020
Oy	1021 TGGAGACTCATCTACATCCACATCTCCCTCATCAACTCCGGAGAAC 1080
Db	1021 TGGAGACTCATCTACATCTCCCTCATCAACTCCGGAGAAC 1080
Oy	1081 TGGCATCTGGCATCCCTCTCTGGGGGGCTGGCTCTGGCTCTGGCAACTCTGGCC 1140
Db	1081 TGGCATCTGGCATCCCTCTGGGGGGCTGGCTCTGGCTCTGGCAACTCTGGCC 1140
Oy	1141 TAACCCATACCTACACATCTGGCTCTGGGGAGATTTGGCT 1200
Db	1141 TAACCCATACCTACACATCTGGCTCTGGGGAGATTTGGCT 1200
Oy	1201 GCTCTTTTCCAGAGAGGGGCCATTACAGATACTGCTGTGGGAATGTCT 1260
Db	1201 GCTCTTTTCCAGAGAGGGGCCATTACAGATACTGCTGTGGGAATGTCT 1260
Oy	1261 TGTGTGTTTTCAGCTACTAGCTCTGGCTCTGGCCAGGTGACCCGGTGTGATGAA 1320
Db	1261 TGTGTGTTTTCAGCTACTAGCTCTGGCTCTGGCCAGGTGACCCGGTGTGATGAA 1320
Oy	1321 GGGAGTTACTCTGGAGAGGCCACCGTGGCCCTCTTAAATAACCGACTTCA 1380
Db	1321 GGGAGTTACTCTGGAGAGGCCACCGTGGCCCTCTTAAATAACCGACTTCA 1380
Oy	1381 ACAGCAGCATCTGGAGGCCAACATTAGGAATGTCAGTAAATATTCT 1440
Db	1381 ACAGCAGCATCTGGAGGCCAACATTAGGAATGTCAGTAAATATTCT 1440
Oy	1441 TCCTTAAGAAACTCTCTGGCTCTGGACTCTTAAAGTGTGTTGAAAT 1500
Db	1441 TCCTTAAGAAACTCTCTGGCTCTGGACTCTTAAAGTGTGTTGAAAT 1500
Oy	1501 GATGTAGTTAAATTATTATACTGGTCTCTACAAAAAAAAAAAAAA 1560
Db	1501 GATGTAGTTAAATTATTATACTGGTCTCTACAAAAAAAAAAAAAA 1560
RESULT 3	
AR228217	
LOCUS	AR228217
DEFINITION	Sequence 5 from patent US 6448005.
ACCESSION	AR228217
VERSION	AR228217..1 GI:2726964
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 1560)
AUTHORS	Gluckmann,M.A. and Tsai,F.-Y.
TITLE	14723 Receptor, a novel G-protein coupled receptor

JOURNAL	Patent: US 6448005-A 5 10-SEP-2002;
FEATURES	Location/Qualifiers
source	1. -1560 /organism="unknown" /mol_type="genomic DNA"
ORIGIN	
Query Match	100.0%; Score 1560; DB 6; Length 1560;
Best Local Similarity	100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 TTGCAACACTCAGCTGGTAAAGCTTCCTCGCAATCTCACAGAGGGGTCAAGGAGTC 60
Db	1 TTGCAACACTCAGCTGGTAAAGCTTCCTCGCAATCTCACAGAGGGGTCAAGGAGTC 60
QY	61 TGCACACCTCAGTGGACCTCCGACTTGCGTTACCGAATTCACAGGGGGTCAAGGAGTC 120
Db	61 TGCACACCTCAGTGGACCTCCGACTTGCGTTACCGAATTCACAGGGGGTCAAGGAGTC 120
QY	121 TCGATGACCTCTGACAGCCCCACAGGGGAGCTCGCCATCTCCGGAGCGCTGG 180
Db	121 TCGATGACCTCTGACAGCCCCACAGGGGAGCTCGCCATCTCCGGAGCGCTGG 180
QY	181 GCGGGGCGCCGGCATGTCGCCCTGAGTGTGCGACAGACAGAGGGGGTCAAGGAGTC 180
Db	181 GCGGGGCGCCGGCATGTCGCCCTGAGTGTGCGACAGACAGAGGGGGTCAAGGAGTC 180
QY	241 CCTGGACAATGCAACCACCTCCCTCTCGATGTCAGGGGACACC 300
Db	241 CCTGGACAATGCAACCACCTCCCTCTCGATGTCAGGGGACACC 300
QY	301 GTGTTGGTGTGAGGTCTGGAGAACCGTTCTGGACTCATCTTGTGTCCTCACTC 360
Db	301 GTGTTGGTGTGAGGTCTGGAGAACCGTTCTGGACTCATCTTGTGTCCTCACTC 360
QY	361 TGGCAACCTGTGCTCTAGTGTGCGGGCCGGCGACCGTGGGGTCAGCC 420
Db	361 TGGCAACCTGTGCTCTAGTGTGCGGGCCGGCGACCGTGGGGTCAGCC 420
QY	421 GCGCTGCTCTAACCTCTCTGGCGGAATTCTCTTACCCGGCATCCCTAGTGC 480
Db	421 GCGCTGCTCTAACCTCTCTGGCGGAATTCTCTTACCCGGCATCCCTAGTGC 480
QY	481 TCGTGTGCGCTGGACTGAGGGCTGGCTGTTGGGGCCCTGGCTGCACTGGCTCT 540
Db	481 TCGTGTGCGCTGGACTGAGGGCTGGCTGTTGGGGCCCTGGCTGCACTGGCTCT 540
QY	541 ACGTGTGACATGAGCCGAGCTCACCATTCTCACACTGGCGGGGTCAGGCTGGAGC 600
Db	541 ACGTGTGACATGAGCCGAGCTCACCATTCTCACACTGGCGGGGTCAGGCTGGAGC 600
QY	601 GCATGTGTCATGTCGCTGGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGAGC 660
Db	601 GCATGTGTCATGTCGCTGGCTGGCGCTGGCGCTGGCGCTGGCGCTGGAGC 660
QY	661 CGGCACTGCTGCTCATGGGTACTGGGCTCCGGCTGGCGCTGGCGCTGGCGCTGGAGC 720
Db	661 CGGCACTGCTGCTCATGGGTACTGGGCTCCGGCTGGCGCTGGCGCTGGAGC 720
QY	721 TGTGCGCTGGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGAGC 780
Db	721 TGTGCGCTGGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGAGC 780
QY	781 TGGATTTGCGCCAAACGGCATAGGAAATCTCGGATGTTGGACTTGAACT 840
Db	781 TGGATTTGCGCCAAACGGCATAGGAAATCTCGGATGTTGGACTTGAACT 840
QY	841 TCTCTGTGCGCCAAACGGCATAGGAAATCTCGGATGTTGGACTTGAACT 900
Db	841 TCTCTGTGCGCCAAACGGCATAGGAAATCTCGGATGTTGGACTTGAACT 900
QY	901 CATGGGGAGAGCTTAGCTGAGCTGGCTGGCTGGCGCTGGCGCTGGAGC 960
Db	901 CATGGGGAGAGCTTAGCTGAGCTGGCTGGCGCTGGCGCTGGAGC 960
QY	951 CCCACACAGACTACCGACTCTTCGAGCTCTCCCTCATCTGTTCTCTCATCA 1020
Db	951 CCCACACAGACTACCGACTCTTCGAGCTCTCCCTCATCTGTTCTCTCATCA 1020
QY	1021 TGTGAGTCCATCATCTCACCATCCCTCTCATCTGTTCTCTCATCA 1080
Db	1021 TGTGAGTCCATCATCTCACCATCCCTCTCATCTGTTCTCTCATCA 1080
QY	1081 TGGTATGTGGCATCCCTTCTCGGTGTTGGCGCTTACGGTCCAACTCTGCC 1140
Db	1081 TGGTATGTGGCATCCCTTCTCGGTGTTGGCGCTTACGGTCCAACTCTGCC 1140
QY	1141 TAACCCATACTGTACACATGTCGCTGTCAGGAAGATGGAGATTTCT 1200
Db	1141 TAACCCATACTGTACACATGTCGCTGTCAGGAAGATGGAGATTTCT 1200
QY	1201 GCTCTTTTCCAGAGGAGGCAATTTCAGAGACGCTGCTGGGGAATGACT 1260
Db	1201 GCTCTTTTCCAGAGGAGGCAATTTCAGAGACGCTGCTGGGGAATGACT 1260
QY	1261 TGCTGTATTCCAGCTTAAGCTTGCGCTTGCCAGGTGAAACACGGTGTGATGAA 1320
Db	1261 TGCTGTATTCCAGCTTAAGCTTGCGCTTGCCAGGTGAAACACGGTGTGATGAA 1320
QY	1321 GGGAGTTACTCAGGAAAGCCACCGTGTGGCCCTCTTTAAATACCGACTCCA 1380
Db	1321 GGGAGTTACTCAGGAAAGCCACCGTGTGGCCCTCTTTAAATACCGACTCCA 1380
QY	1381 ACAGCAGGCACTACGGGCCGAATTAAGAATGCTGCTGAGTTAAATATT 1440
Db	1381 ACAGCAGGCACTACGGGCCGAATTAAGAATGCTGCTGAGTTAAATATT 1440
QY	1441 TCCTTAAGAAGACTTCTATGGTTCTTGTGACTTTAACTGTTGTAAT 1500
Db	1441 TCCTTAAGAAGACTTCTATGGTTCTTGTGACTTTAACTGTTGTAAT 1500
QY	1501 GATCTAGTTATAATTATTATAAGTGTCTCACAMAAAAAAA 1560
Db	1501 GATCTAGTTATAATTATTATAAGTGTCTCACAMAAAAAAA 1560
QY	1560
RESULT 4	
AR372102	
LOCUS	AR372102
DEFINITION	Sequence 5 from patent US 6395877.
ACCESSION	AR372102
VERSION	AR372102..1 GI:34609379
KWDS	
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 1560)
AUTHORS	Gluckmann, M.A. and Tsai, F.-Y.
TITLE	14273 receptor, a novel G-protein coupled receptor
JOURNAL	Patent: US 6395877-A 5 28-MAY-2002;
FEATURES	Location/Qualifiers
source	1. -1560 /organism="unknown" /mol_type="genomic DNA"
ORIGIN	
Query Match	100.0%; Score 1560; DB 6; Length 1560;
Best Local Similarity	100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 TTGCAACACTCAGCTGGTAAAGCTTCCTCGCAATCTCACAGGGGTCAAGGAGTC 60
Db	1 TTGCAACACTCAGCTGGTAAAGCTTCCTCGCAATCTCACAGGGGTCAAGGAGTC 60
QY	61 TTGCAACACTCAGCTGGTAAAGCTTCCTCGCAATCTCACAGGGGTCAAGGAGTC 120

Db	61	TTCACACCATCGTAGGACCACTCCAGACTTGTCCGCCTTACCGAATCTTCACAGGGGG	120
Qy	121	TCGTGACCTCTTGACAGCCACGGGGGAACTCCGCATCTCCGGAGGGTGG	180
Db	121	TCTGTGACCTCTTGACAGCCACGGGGGAACTCCGCATCTCCGGAGGGTGG	180
Qy	181	GCGCGGCGCCGATGRCCTGAGTGTGAGCAGACGAGGAGGGGCGAGCTCGCAC	240
Db	181	GCGCGGCGCCGATGTCCTCTTGAGTGTGAGCAGACGAGGAGGGGCGAGCTCGCAC	240
Qy	241	CCTCTGACCAAATGCCAATCCACCACTTCCCTTCTTGAGTGTGAGCAGGAGACC	300
Db	241	CCTCTGACCAAATGCCAATCCACCACTTCCCTTCTTGAGTGTGAGCAGGAGACC	300
Qy	301	GTTGGTGTGAGGCTGTCAGTGTGAGTGTGAGCAGACGAGGAGGGGACACC	360
Db	301	GTTGGTGTGAGGCTGTCAGTGTGAGCAGACGAGGAGGGGACACC	360
Qy	361	TGGGCAACCTGTGTCCTAGTGTGAGGACACCGTCTGGAGCTATCTGTGTCAC	420
Db	361	TGGGCAACCTGTGTCCTAGTGTGAGGACACCGTCTGGAGCTATCTGTGTCAC	420
Qy	421	GCGCTGTCTCAACCTCTCTGGCGGAGTGTGAGCTTCTGGAGCTTCTGGAGCT	480
Db	421	GCGCTGTCTCAACCTCTGGAGCTTCTGGAGCTTCTGGAGCTTCTGGAGCT	480
Qy	481	TCTGTGAGGCTGACTGAGGGCTGGCTTGGGCCCCCTGTGTGCCACCTGCTCT	540
Db	481	TCTGTGAGGCTGACTGAGGGCTGGCTTGGGCCCCCTGTGTGCCACCTGCTCT	540
Qy	541	ACGGTACATGAGCCGAGCTCAGCTGGCTTGGGCCCCCTGTGTGCCACCTGCT	600
Db	541	ACGGTACATGAGCCGAGCTCAGCTGGCTTGGGCCCCCTGTGTGCCACCTGCT	600
Qy	601	GCTGGTGTGAGCATGTCGGCTTGGGCCCCCTGTGTGCCACCTGCT	660
Db	601	GCTGGTGTGAGCATGTCGGCTTGGGCCCCCTGTGTGCCACCTGCT	660
Qy	661	CGGACTCTGTGTTCATGGGTACTCGGGCTCGGGGCTGGGACTCGCCCTAC	720
Db	661	CGGACTCTGTGTTCATGGGTACTCGGGCTCGGGGCTGGGACTCGCCCTAC	720
Qy	721	TGTCCGGGTGTCGGCTCCGGGGACCGAATTGGATTCGAGATTCGAGAT	780
Db	721	TGTCCGGGTGTCGGCTCCGGGGACCGAATTGGATTCGAGATTCGAGAT	780
Qy	.781	TGATGGGCCAACCGCATAGGAAATCTCATGGATGTGTTTGAGCTTGA	840
Db	.781	TGATGGGCCAACCGCATAGGAAATCTCATGGATGTGTTTGAGCTTGA	840
Qy	841	TCTGTGAGGACTGTGATCAGTACTCCAATTAGACGACGAAG	900
Db	841	TCTGTGAGGACTGTGATCAGTACTCCAATTAGACGACGAAG	900
Qy	901	CTCGCGGAAAGGGCTAGCTTGATCAGTACTCCAATTAGACGACGAAG	960
Db	901	CTCGCGGAAAGGGCTAGCTTGATCAGTACTCCAATTAGACGACGAAG	960
Qy	961	CCACACAGACTACCGACTCTGGAGCTGATCAAACCTCCGAGGAC	1020
Db	961	CCACACAGACTACCGACTCTGGAGCTGATCAAACCTCCGAGGAC	1020
Qy	1021	TGGGACTCCATCATCACCTCTGATCAAACCTCCGAGGAC	1080
Db	1021	TGGGACTCCATCATCACCTCTGATCAAACCTCCGAGGAC	1080
Qy	1081	TGGTCACTGGCCATCCCTTCTGGGCTTCTGAGCTTGCCAACTCTGC	1140
Db	1081	TGGTCACTGGCCATCCCTTCTGGGCTTCTGAGCTTGCCAACTCTGC	1140
Qy	1141	TAACCCCATATGTCACATCTGGTACGAGAATGGAGGAGATTTGCT	1200
Db	1141	TAACCCCATATGTCACATCTGGTACGAGAATGGAGGAGATTTGCT	1200

		RESULT 5	
		BC053698	
Locus		BC053698	1419 bp mRNA linear ROD 12-Nov-2003
DEFINITION		Mus musculus G protein-coupled receptor 120, mRNA (cDNA clone MGC:22870 IMAGE:6529120)	complete cds.
ACCESSION		BC053698	BC053698.1 GI:31566089
VERSION			
AUTHORS			
SOURCE		Mus musculus (house mouse)	
ORGANISM		Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murida; Mus.	
REFERENCE		(bases 1 to 1419)	
Strausberg, R.L., Fengold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, P.S., Wagner, L., Scheuer, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Butow, K.H., Schaefer, C.F., Bhattacharya, R.P., Jordan, H., Moore, T., Max, S.I., Wang, J., Heile, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Cabavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiroki, S., Carninci, P., Prange, C., Raha, S.S., Lognelli, N.A., Peters, G.J., Abramson, R.D., Mulhall, S.J., Bosak, S.A., McEwan, P.J., McNernan, K.J., Malek, J.A., Bosak, S.A., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Keeteman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shvchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimes, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smilis, D.E., Schnarch, A., Schein, J.E., Jones, S.J. and Marra, M.A.			
REMARK		human and mouse cDNA sequences	Submitted (09-Jun-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
COMMENT		2 (bases 1 to 1419)	NIH-MGC Project URL: http://mgc.nci.nih.gov
		Authors	Contact: MGC help desk Email: craps@mail.nih.gov
		Title	Tissue Procurement: Jeffrey B. Green, M.D.
		Journal	JOURNAL
		Medline	Submitted (09-Jun-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
		Pubmed	22380257
		Reference	1247932
		Author	Strausberg, R.
		Title	Direct Submission
		Journal	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
		Medline	Submitted (09-Jun-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
		Pubmed	1247932
		Reference	(bases 1 to 1419)
		Author	Strausberg, R.
		Title	JOURNAL
		Journal	Submitted (09-Jun-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
		Medline	22380257
		Reference	1247932
		Author	Strausberg, R.
		Title	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
		Journal	Submitted (09-Jun-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
		Medline	22380257
		Reference	1247932
		Author	Strausberg, R.
		Title	JOURNAL
		Journal	Submitted (09-Jun-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
		Medline	22380257
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		Medline	22380257

Contact: nisc.msc@negr.nih.gov
 CDNA library preparation: Life Technologies, Inc.
 DNA library Arrayed by: The I.M.A.G.E. Consortium (LNU)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: http://www.nisc.nih.gov/

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNU at: http://image.lnl.gov

Series: TRAK Plate: 116 Row: n Column: 18.

FEATURES	source	Location/Qualifiers	gene	CDS
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QY	231 CCCTCCACACCTGGACCAAGTCAATCGAACCCACTTCCCTCTCGATGTCAAG 290			
Db	85 CCTCCACACCTGGACCAAGTCAATCGAACCCACTTCCCTCTCGATGTCAAG 144			
Qy	291 GGCGACGACCGGTGTTGTTGAGCGTGTGAGCAGCACCGTCTGTCAGTCACTTGTC 350			
Db	145 GCGGACGACCGGTGTTGAGCGTGTGAGCAGCACCGTCTGTCAGTCACTTGTC 204			
Qy	351 GTCTCTGTCTGGGACAGTGTGTCTAGTGCTGTGGGGGGCTGGGGCTGGGGCTGG 410			
Db	205 GTCTCTGTCTGGGACAGTGTGTCTAGTGCTGTGGGGCTGGGGCTGGGGCTGG 264			
Qy	411 GGCTGAGGCCAGGCTGGCTCACCTTCTCGCGCGATGTCCTCACAGCGCATC 470			
Db	265 GGAGACGCCAGGCTGGCTCACCTTCTCGCGCGATGTCCTCACAGCGCATC 324			
RESULTS	6			
AY288424	AY288424	1086 bp mRNA linear ROD 08-DEC-2003		
LOCUS				
VERSION				

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ACCESSION	AY288424		397	AGCTGGAGCGCATGGTTCGATGTGCGCCTCGGCCGGCTGAGGCGCCCGGGGG	456
VERSION	AY288424.1				
KEYWORDS					
SOURCE	Mus musculus (house mouse)		651	CGACTCGGGGCACTGCTGGCTTCA-TGSGGTTCTCGGGCTCGGGCTCCGGG	710
ORGANISM	Mus musculus				
REFERENCE	1 (bases 1 to 1086)		457	CGGACTCGGGGCACTGCTGGCTTCA-TGSGGTTCTCGGGCTCGGGCTCCGGG	516
AUTHORS	Fredriksson, R., Hoglund, P.J., Gloriam, D.E., Lagerstrom, M.C. and Schioth, H.B.		711	CTCTACACTTGTCGGTGGCCGGAGGCCTCCGGGGAGCAGGAATTGG	770
TITLE	Seven evolutionarily conserved human rhodopsin G protein-coupled receptors lacking close relatives				
JOURNAL	FEBS Lett. 554 (3), 381-388 (2003)				
MEDLINE	22985413				
PUBMED	14623098				
REFERENCE	2 (bases 1 to 1086)		1. .1086	/organism="Mus musculus"	
AUTHORS	Fredriksson, R., Hoglund, P.J., Gloriam, D.E.I., Lagerstrom, M.C. and Schioth, H.B.			/mol type="mRNA"	
JOURNAL	Submitted (30-APR-2003) Neuroscience; Unit of Pharmacology, Uppsala University, Box 593, Uppsala 75124, Sweden		1. .1086	/db_xref="taxon:10090"	
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Query Match	47.7%		QY	591 AGCTTGAGGCGCATGTGCGATCGCCCTCGGCCGGCTGAGGCGCCCGGGGG	650
Best Local Similarity	99.4%		Db	397 AGCTGGAGCGCATGGTTCGATGTGCGCCTCGGCCGGCTGAGGCGCCCGGGGG	456
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Conservative	0;		Db	457 CGGACTCGGGGCACTGCTGGCTTCA-TGSGGTTCTCGGGCTCGGGCTCCGGG	516
Mismatches	0;		QY	711 CTCTACACTTGTCGGTGGCCGGAGGCCTCCGGGGAGCAGGAATTGG	770
Indels	6;		Db	517 CTCTACACTTGTCGGTGGCCGGAGCAGGAATTGG	576
Gaps	0;		QY	771 ATTCGACATTGGATGSCGCCAACGCGATAGGAGAATTCAG	830
			Db	577 ATTCGACATTGGATGSCGCCAACGCGATAGGAGAATTCAG	636
			QY	831 ACTTGAAGTCCCGGCGCGACTGCTAGTGTAGCACTCTGAGCAGTACTCCAAATTAG	890
			Db	637 ACTTGAAGTCCCGGCGACTGCTAGTGTAGCACTCTGAGCAGTACTCCAAATTAG	696
			QY	891 ATCACGAAAGCATGGCGAGAGCTTACGTGAGCTGAGCCACCG	950
			Db	697 ATCACGAAAGCATGGCGAGAGCTTACGTGAGCTGAGCTGAGCAGGCCACCG	756
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			Db	757 ATCCGAGGTTCCAAACAAAGACTACCGACTCTCCGCGACGCTCTCCCTCATGTTCC	816
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			Db	817 TTCTCATCATGTTGAGCCATCATCACCATTCTCTCATCTGTTCACTCAAACCTTC	876
			QY	1071 CGGAGGACTGGTCACTGGCCATCCCTTCTGGTGTGGCTTCAGTTGCC	1130
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LOCUS	AC112153				
DEFINITION	Mus musculus BAC clone RP24-93G11 from chromosome 19, complete sequence.				
VERSION	AC112153				
KEYWORDS	HTG.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 18094)				
AUTHORS	Tomlinson, C. and Hoglund, K.				
TITLE	The sequence of Mus musculus BAC clone RP24-93G11				
JOURNAL	Unpublished (2001)				
REFERENCE	2 (bases 1 to 18094)				
AUTHORS	Wilson, R.				
TITLE	Sequencing of <i>Mus musculus</i>				
JOURNAL	Unpublished (2001)				
REFERENCE	3 (bases 1 to 18094)				
AUTHORS	McPherson, J.D. and Waterston, R.H.				
TITLE	Direct Submission				
JOURNAL	Submitted (19-FEB-2002) Genome Sequencing Center, 4444 Forest Park				

REFERENCE Parkway, St. Louis, MO 63108, USA
 4 (bases 1 to 18094)
 AUTHORS Wilson, R.K.
 TITLE Direct Submission
 JOURNAL Submitted (15-MAY-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 5 (bases 1 to 18094)
 AUTHORS Wilson, R.K.
 TITLE Direct Submission
 JOURNAL Submitted (06-SEP-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 6 (bases 1 to 18094)
 AUTHORS Wilson, R.
 TITLE Direct Submission
 JOURNAL Submitted (27-NOV-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Sep 6, 2003 this sequence version replaced gi:30725984.

COMMENT ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUSSC
 Web site: <http://genome.wustl.edu>
 Contact: submissions@atson.wustl.edu

----- Summary Statistics
 Center project name: M_BB093G11

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
 Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

SOURCE INFORMATION:
 The RCI-24 BAC library has been constructed by Pieter de Jong and coworkers (<http://www.chori.org>) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at <http://www.chori.org>

NEIGHBORING SEQUENCE INFORMATION:
 This sequence is the entire insert of the clone.

FEATURES

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 repeat_region 15271. -15372 /rpt_family="Alu"
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 unsure 17326. -17397 /note="Sequence derived from one plasmid subclone."
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 repeat_region 26526. -26557 /rpt_family="MER2_type"
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Smith, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: Sequence_Submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: Li7381
 Center clone name: 113J17
 ----- Summary Statistics
 Sequencing vector: Plasmid n/a: 10% of reads
 Chemistry: Dye-terminator Big Dye: 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 233359 bases at least Q40
 Consensus quality: 235646 bases at least Q30
 Consensus quality: 236645 bases at least Q20
 Insert size: 210000; agarose-fp
 Insert size: 237818; sum-of-contigs
 Quality coverage: 9.1 in Q20 bases; agarose-fp
 Quality coverage: 8.1 in Q20 bases; sum-of-contigs
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 20 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 309: contig of 309 bp in length
 310 409: gap of 100 bp
 409 1476: contig of 1067 bp in length
 1477 1376: gap of 100 bp
 1376 1577: contig of 1177 bp in length
 1577 2753: gap of 100 bp
 2753 3880: contig of 1027 bp in length
 3881 3980: gap of 100 bp
 3981 5036: contig of 1056 bp in length
 5037 5137: gap of 100 bp
 5137 6296: contig of 1160 bp in length
 6296 6396: gap of 100 bp
 6396 7884: contig of 1488 bp in length
 7885 7984: gap of 100 bp
 7984 9675: contig of 1590 bp in length
 9675 9775: gap of 100 bp
 9775 10982: contig of 1207 bp in length
 10982 11081: gap of 100 bp
 11082 13248: contig of 2166 bp in length
 13248 13347: gap of 100 bp
 13347 16735: contig of 3387 bp in length
 16735 16834: gap of 100 bp
 16834 23539: contig of 6705 bp in length
 23539 23640: gap of 100 bp
 23640 23987: contig of 5747 bp in length
 23987 29466: gap of 100 bp
 29466 29487: contig of 14329 bp in length
 29487 43915: gap of 100 bp
 43915 55354: contig of 11439 bp in length
 55354: gap of 100 bp
 54455 82497: contig of 27043 bp in length
 82497 82498: gap of 100 bp
 82498 109789: contig of 21201 bp in length
 109789 109898: gap of 100 bp
 109898 181806: contig of 71908 bp in length
 181806 181906: gap of 100 bp
 181906 181907: contig of 31267 bp in length
 181907 213174: gap of 100 bp
 213174 233723: contig of 26445 bp in length.
 233723 LocationQualifiers
 1. -239718 /organism="Mus musculus"
 /mol_type="genomic DNA"

	AUTHORS	TITLE
QY	Gluckmann,M.A. and Tsai,F.-Y.	JOURNAL
Db	100859 AGATTTTGCTCTTTCAGAGGAGCATTACAGATCTCTGTC	Patent: US 6448005-A 15-SEP-2002;
QY	1248 AGCCGAATGACTGTCTTATTCAGAAGGAGCATTACAGATCTCTGTC	Location/Qualifiers
Db	100918 AGCCGAATGACTGTCTTATTCAGAAGGAGCATTACAGATCTCTGTC	source 1..118 /organism="unknown" /mol_type="genomic DNA"
QY	1308 GCTGCGATGACTGTCTTATTCAGAAGGAGCATTACAGATCTCTGTC	ORIGIN
Db	100978 GCTGCGATGACTGTCTTATTCAGAAGGAGCATTACAGATCTCTGTC	Query Match 8.8%; Score 138; DB 6; Length 138; Best Local Similarity 100.0%; Pred. No. 4.9e-69; Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1368 TACCCGACTCCCAACAGCAGGATCTACGGCAGCAATTAGGATGACTCTAGT	Matches 1427
Db	101018 TACCCGACTCCCAACAGCAGGATCTACGGCAGCAATTAGGATGACTCTAGT	101097
QY	1428 ATAAAATATTTCCTTAAGAAGACTTCTATGGTCTCTTGGAATT 1483	QY 909 AACAGGCTTACGCGAGCTGCACTCTGAGAGCCACAGCCGAGTCACAA 968 Db 1 AAGAGCTTACGCGAGCTGCACTCTGAGAGCCACAGCCGAGTCACAA 60
Db	101098 ATAAAATATTTCCTTAAGAAGACTTCTATGGTCTCTTGGAATT 101153	QY 969 GACTCCACTCTCGAGCTTCTGCTATGGTCTCTCATCTGGT 1028 Db 61 GACTCCACTCTCGAGCTTCTGCTATGGTCTCTCATCTGGT 120
RESULT 9	AR228218 AR228218 181 bp DNA linear PAT 20-DEC-2002	QY 1029 CCCATCATCATCACCATC 1046 Db 121 CCCATCATCATCACCATC 138
LOCUS	AR228218	DEFINITION Sequence 14 from patent US 6448005.
VERSION	AR228218.1	ACCESSION GI:27266965
KEYWORDS	ORGANISM Unknown.	SOURCE
SOURCE	Unclassified.	ORGANISM
REFERENCE	1 (bases 1 to 181)	DEFINITION
AUTHORS	Gluckmann,M.A. and Tsai,F.-Y.	LOCUS BC049237
TITLE	1473 Receptor, a novel G-protein coupled receptor	DEFINITION Mus musculus electron transfer flavoprotein, beta polypeptide, mRNA (cDNA clone MGC:54845 IMAGE:4241552), complete cds.
JOURNAL	Patent: US 6448005-A 14-10-SEP-2002;	ACCESSION BC049237
FEATURES	Source	VERSION BC049237.1
	Location/Qualifiers	KEYWORDS MGC.
ORIGIN	Query Match 11.6%; Score 181; DB 6; Length 181; Best Local Similarity 100.0%; Pred. No. 2.7e-94; Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	AUTHORS
QY	1021 TGTGAGGCCATCATCATCACCACTCCMCCTCTACTGATCCAAACTTCCCGCAGGCC	REFERENCE
Db	1 TGTGAGGCCATCATCATCACCACTCCMCCTCTACTGATCCAAACTTCCCGCAGGCC	1080
QY	1081 TGTGAGGCCATCATCATCACCACTCCMCCTCTACTGATCCAAACTTCCCGCAGGCC	AUTHORS
Db	61 TGTGAGGCCATCATCACCACTCCMCCTCTACTGATCCAAACTTCCCGCAGGCC	Klausner,R.D., Collins,F.S., Wagner,L., Scheuer,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Butow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Smeal,P., Prange,C., Raha,S.S., Lognallano,N.A., Peters,G.J., Stapleton,M., Soares,M.B., Bonald,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T., Toshiriki,S., Carninci,P., Abramson,R.D., Mulhall,S.J.J., Bosak,S.A., McLean,P.J., Abramson,R.D., Mulhall,S.J.J., Bosak,S.A., McLean,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Soedergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Keeteman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shvchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalius,D.E., Schnarch,A., Schein,J.E., Jones,S.J. and Matra,M.A.
QY	1141 TAACTCTATGCTACAGCTGGCTTCTGGAGAGATTTCCT	TITLE
Db	121 TAACTCTATGCTACAGCTGGCTTCTGGAGAGATTTCCT	JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
QY	1201 G 1201	PUBLISHED MEDLINE 22380257
Db	181 G 181	REFERENCE
RESULT 10	AR228219 AR228219 138 bp DNA linear PAT 20-DEC-2002	AUTHORS Strausberg,R.
LOCUS	AR228219 Sequence 15 from patent US 6448005.	TITLE Direct Submission
DEFINITION		JOURNAL Submitted (21-Mar-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
ACCESSION	AR228219.1 GI:27266966	REMARK NIH/MGC Project URL: http://mgc.nci.nih.gov
KEYWORDS	Unknown.	COMMENT Contact: MGC help desk Email: mgcsupport@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D.
ORGANISM	Unclassified.	REFERENCE 1 (bases 1 to 138)
REFERENCE		

NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone.

NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone.

FEATURES	Location/Qualifier	Source	repeat_region	/note="Sequence derived from one plasmid subclone."
source			repeat_region	18359..18501 /RPT family="Alu"
			repeat_region	18311..19194 /RPT family="L1"
			repeat_region	19246..19380 /RPT family="B2"
			repeat_region	19381..19425 /RPT family="B4"
			repeat_region	19600..19790 /RPT family="B2"
			repeat_region	19869..20088 /RPT family="B2"
			repeat_region	20115..20270 /RPT family="B4"
			repeat_region	20581..20778 /RPT family="L1"
			repeat_region	21094..21166 /RPT family="B2"
			repeat_region	21128..21307 /RPT family="B4"
			repeat_region	21301..21491 /RPT family="L1"
			repeat_region	21499..21743 /RPT family="B2"
			repeat_region	21822..22007 /RPT family="B4"
			repeat_region	22126..22216 /RPT family="B4"
			repeat_region	22839..24140 /RPT family="L1"
			repeat_region	25383..25460 /RPT family="ID"
			repeat_region	25388..25456 /RPT family="ID"
			repeat_region	/product="tRNA-Ala"
			repeat_region	/note="Likely pseudogene (HMM Sc=34.12 / Sec struct SC1.92)"
			repeat_region	26997..27316 /RPT family="ERVL"
			repeat_region	27476..27572 /RPT family="Alu"
			repeat_region	28060..28287 /RPT family="L12"
			repeat_region	28441..28607 /RPT family="MalR"
			repeat_region	28552..28828 /RPT family="MalR"
			repeat_region	28829..29172 /RPT family="MalR"
			repeat_region	29173..29340 /RPT family="MalR"
			repeat_region	29420..29503 /RPT family="B4"
			repeat_region	29504..29635 /RPT family="Alu"
			repeat_region	/rpt family="B2"
			repeat_region	1881..12020 5.9%; Score 92; DB 10; Length 169206; Best Local Similarity 100.0%; Pred. No. 1.6e-41; Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
			repeat_region	13831..13978 /rpt family="L1"
			repeat_region	13979..14312 /rpt family="L1"
			repeat_region	14317..14730 /rpt family="L1"
			repeat_region	14731..14915 /rpt family="B2"
			repeat_region	14916..14967 /rpt family="L1"
			repeat_region	1616..16585 /rpt family="L1"
			repeat_region	17108..18100 /rpt family="L1"
			repeat_region	18285..18307 /rpt family="L1"

RESULT 13
AC079543 LOCUS AC079543 DNA linear HTG 02-SEP-2000
DEFINITION Mus musculus clone RP23-381P16, WORKING DRAFT SEQUENCE, 67
QY 7B CACTCCAGACTTGCGGGTTACCGGAATT 109
Db 80518 AGCCCTCTTCACTGCAATCAGACAGAGGGTTCACTGAC 77
QY 7B CACTCCAGACTTGCGGGTTACCGGAATT 109
Db 80458 CACTCCAGACTTGCGGGTTACCGGAATT 80427
unsure

ACCESSION * * * * *
VERSION AC079543
KEYWORDS REFERENCE * * * * *
HTG; HTGS; PHASEL; HTGS_DRAFT.
AUTHORS * * * * *
Mus musculus (house mouse)
ORGANISM * * * * *
Bukayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butchia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE * * * * *
1 (bases 1 to 277603)
AUTHORS * * * * *
DOE Joint Genome Institute.
TITLE * * * * *
Sequencing of Mouse
JOURNAL * * * * *
unpublished
COMMENT * * * * *
2 (bases 1 to 277603)
AUTHORS * * * * *
DOB Joint Genome Institute.
TITLE * * * * *
direct Submission
JOURNAL * * * * *
Submitted (02-SEP-2000) Production Sequencing Facility, DOE Joint
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 1883552
Center clone name: RPCI-23_381p16

Summary Statistics
Consensus quality: 224010 bases at least Q40
Consensus quality: 249280 bases at least Q30
Consensus quality: 255396 bases at least Q20
Estimated insert size: 172000; agarose-fp estimation
Estimated insert size: 271003; sum-of-contigs estimation
Quality coverage: 6.92 in Q20 bases; agarose-fp estimation
Quality coverage: 4.39 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a working draft sequence. It currently
* consists of 67 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* * * * *
1 1043: contig of 1043 bp in length
1044 1143: gap of unknown length
1144 2187: contig of 1044 bp in length
* * * * *
2188 2287: gap of unknown length
2288 3468: contig of 1181 bp in length
* * * * *
3469 3568: gap of unknown length
3569 4840: contig of 1272 bp in length
4841 4940: gap of unknown length
4941 6012: contig of 1072 bp in length
* * * * *
6013 6112: gap of unknown length
6113 7304: contig of 1192 bp in length
7305 7404: gap of unknown length
* * * * *
7405 8702: contig of 1298 bp in length
8703 8802: gap of unknown length
* * * * *
8803 1001: contig of 1199 bp in length
1002 10101: gap of unknown length
* * * * *
10101 11249: contig of 1148 bp in length
11250 11349: gap of unknown length
* * * * *
11350 12629: contig of 1280 bp in length
12630 12729: gap of unknown length
* * * * *
12730 13945: contig of 1216 bp in length
* * * * *
13946 14045: gap of unknown length
* * * * *
14046 15833: contig of 1788 bp in length
* * * * *
15834 15933: gap of unknown length
* * * * *
15934 17862: contig of 1929 bp in length
17863 17962: gap of unknown length
* * * * *
17963 18991: contig of 1029 bp in length
* * * * *
18992 19091: gap of unknown length
* * * * *
19092 20898: contig of 1807 bp in length
20899 22832: gap of unknown length
* * * * *
22833 22932: gap of unknown length
22933 24144: contig of 1212 bp in length
24144 24244: gap of unknown length
24245 25659: contig of 1225 bp in length
25670 25770: gap of unknown length
27229: contig of 1470 bp in length
* * * * *
27240 27319: gap of unknown length
27340 28790: contig of 1451 bp in length
28791 28890: gap of unknown length
* * * * *
28891 30106: contig of 1216 bp in length
30107 30205: gap of unknown length
* * * * *
30207 31602: contig of 1396 bp in length
* * * * *
31603 31702: gap of unknown length
31703 32867: contig of 1165 bp in length
32868 32968: gap of unknown length
* * * * *
34417 34515: gap of unknown length
34517 35577: contig of 1061 bp in length
35578 35677: gap of unknown length
35678 37248: contig of 1449 bp in length
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37249 37348: gap of unknown length
* * * * *
37349 38610: contig of 1262 bp in length
* * * * *
38611 38710: gap of unknown length
* * * * *
38711 38789: contig of 1679 bp in length
* * * * *
40390 40489: gap of unknown length
40490 41593: contig of 1104 bp in length
41594 41694: gap of unknown length
* * * * *
41694 43102: contig of 1409 bp in length
43103 43202: gap of unknown length
* * * * *
43202 44777: contig of 1575 bp in length
44778 44788: gap of unknown length
44878 45440: contig of 1563 bp in length
* * * * *
45441 46540: gap of unknown length
46541 46541: contig of 2069 bp in length
* * * * *
46541 48609: contig of 1402 bp in length
48609 48709: gap of unknown length
* * * * *
48710 49895: contig of 1186 bp in length
49895 49995: gap of unknown length
* * * * *
49995 50524: contig of 1511 bp in length
50524 51506: gap of unknown length
* * * * *
51507 51606: gap of unknown length
51607 53008: contig of 2043 bp in length
* * * * *
53008 53108: gap of unknown length
53108 53109: contig of 1186 bp in length
* * * * *
53109 55141: gap of unknown length
55141 55240: gap of unknown length
55241 55760: contig of 2520 bp in length
* * * * *
55761 57860: gap of unknown length
* * * * *
57861 59903: contig of 2043 bp in length
* * * * *
59904 60003: gap of unknown length
* * * * *
60004 62375: contig of 2372 bp in length
* * * * *
62375 62475: gap of unknown length
62475 64891: contig of 2416 bp in length
* * * * *
64892 64991: gap of unknown length
* * * * *
64992 67699: contig of 2708 bp in length
* * * * *
67699 67799: gap of unknown length
* * * * *
67799 67800: contig of 1825 bp in length
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67800 69624: contig of 1825 bp in length
* * * * *
69625 69725: gap of unknown length
* * * * *
69725 71722: contig of 1998 bp in length
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71722 71822: gap of unknown length
* * * * *
71823 75072: contig of 3250 bp in length
* * * * *
75072 75172: gap of unknown length
* * * * *
75172 77256: contig of 2084 bp in length
* * * * *
77256 77356: gap of unknown length
* * * * *
77357 77357: contig of 2446 bp in length
* * * * *
77357 79803: gap of unknown length
* * * * *
79803 79902: gap of unknown length
* * * * *
79902 79903: contig of 1819 bp in length
* * * * *
79903 81721: contig of 1819 bp in length
* * * * *
81721 81722: gap of unknown length
* * * * *
81722 86203: contig of 4382 bp in length
* * * * *
86203 86303: gap of unknown length
* * * * *
86304 92047: contig of 5744 bp in length
* * * * *
92048 92147: gap of unknown length
* * * * *
92148 95857: contig of 3710 bp in length
* * * * *
95857 95957: gap of unknown length
* * * * *
95958 99755: contig of 3798 bp in length
* * * * *

99856 104254: contig of 4399 bp in length
 * 104255 104354: gap of unknown length
 * 104355 108546: contig of 4192 bp in length
 * 108547 108646: gap of unknown length
 * 108647 113196: contig of 4550 bp in length
 * 113197 113296: gap of unknown length
 * 113297 119952: contig of 6656 bp in length
 * 119953 120052: gap of unknown length
 * 120053 121219: contig of 1167 bp in length
 * 121220 121311: gap of unknown length
 * 121320 129289: contig of 7970 bp in length
 * 129290 129390: gap of unknown length
 * 129391 139139: contig of 9749 bp in length
 * 139139 139238: gap of unknown length
 * 139239 151545: contig of 12307 bp in length
 * 151546 151645: gap of unknown length
 * 151646 162316: contig of 10671 bp in length
 * 162317 162416: gap of unknown length
 * 162417 174418: contig of 12002 bp in length
 * 174419 174518: gap of unknown length
 * 174519 192093: contig of 17575 bp in length
 * 192094 192193: gap of unknown length
 * 192194 212136: contig of 1943 bp in length
 * 212137 212236: gap of unknown length
 * 212237 223430: contig of 21194 bp in length
 * 223431 223530: gap of unknown length
 * 223531 259553: contig of 26023 bp in length
 * 259554 259653: gap of unknown length
 * 259654 277603: contig of 17950 bp in length.
FEATURES
SOURCE

1. .277603 Qualifiers location

/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="Taxon:1090"
/clone="RP3-381p16"
/clone_lib="RPCI mouse BAC library 23"

ORIGIN

Query Match Score 92; DB 2; Length 277603;

Best Local Similarity 100.0%; Pred. No. 1.8e-41; Mismatches 0; Indels 0; Gaps 0;

Matches 92; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 18 AGCTCTTCACTGCAATCTCAGAGGGTCTAGGGTCTCACCCATCAGTCACCTGCACT 77
Db 250130 AGCTCTTCACTGCAATCTCAGAGGGTCTAGGGTCTCACCCATCAGTCACCTGCACT 250189
Qy 78 CACTCCAGACTTGCCGACTTACCCGAATCT 109
Db 250190 CACTCCAGACTTGCCGACTTACCCGAATCT 250221**RESULT 14**

AC080156 AC080156 212822 bp DNA linear HTGS 09-OCT-2002
DEFINITION Ratius norvegicus clone RP32-379B20, *** SEQUENCING IN PROGRESS
ACCESSION *** 8 unordered pieces.
VERSION AC00156
KEYWORDS HTG; HTGS; PHAGE; HTGS DRAFT; HTGS_ENRICHED.
SOURCE Ratius norvegicus (Norway rat)

ORGANISM Ratius norvegicus
MATERIALS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Elteleostomi;
AUTHORS Rattus.
REFERENCE 1 (bases 1 to 212822)
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REFERENCE 1 (bases 1 to 212822)

REFERENCE 1 (bases 1 to 212822)

REFERENCE 1 (bases 1 to 212822)

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REFERENCE 1 (bases 1 to 212822)

REFERENCE 1 (bases 1 to 212822)

Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Diu,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Barnhart,C., Edgar,O., Edwards,C.C., Elmaj,C., Escott,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudh,S., Karlsson,E., Kelly,S., Khan,U., King,L., Kovar,J., Kovar,C., Kratoric,J., Korean,A., Landy,N., Leahy,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louiseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapus,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhinney,B., McLeod,M.P., Meador,M., Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,M., Mohabat,K., Morgan,M., Morgan,M., Moser,M., Neal,D., Newtonson,J., Newson,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokonkwuo,S., Oguh,M., Okwuonu,G., Oragunye,N., Oriello,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.I., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojibukan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshani,N., Sison,I., Sodergren,E., Sonnleit,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerska,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,J., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczik,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.

TITLE Direct Submission
JOURNAL Direct Submission
REFERENCE Unpublished
AUTHORS 2 (bases 1 to 212822)
TITLE Direct Submission
JOURNAL Submitted (27-SEP-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 212822)
AUTHORS 2 (bases 1 to 212822)
TITLE Direct Submission
JOURNAL Submitted (09-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT On Sep 23, 2002 this sequence version replaced gi:2193372. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/proj/rat/>). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence only reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: TUAB
Center clone name: Rp32-379B20
----- Summary Statistics
Assembly program: Phrap; version 0.90329
Consensus quality: 196316 bases at least Q40
Consensus quality: 197975 bases at least Q30
Estimated insert size: 222120; sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
* NOTE: This is a 'working draft' sequence. It currently

* consists of 8 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1. 13733: contig of 13733 bp in length
 * 13734 13833: gap of unknown length
 * 13834 202133: contig of 183300 bp in length
 * 202134 202233: gap of unknown length
 * 202234 205371: contig of 3138 bp in length
 * 205372 205471: gap of unknown length
 * 205472 206631: contig of 1160 bp in length
 * 206632 206731: gap of unknown length
 * 206732 20785: contig of 1136 bp in length
 * 207870 207969: gap of unknown length
 * 207970 20984: contig of 1115 bp in length
 * 20985 209184: gap of unknown length
 * 210652: contig of 1468 bp in length
 * 210653 210752: gap of unknown length
 * 210753 212822: contig of 2070 bp in length.

FEATURES

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 /note="wgs contig"
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 /note="wgs contig"
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Query Match 4.9%, score 77, DB 2, Length 212822;
 Best local Similarity 100.0%, Pred. No. 1.e-32;
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 987 ACCTCTCTCTGCATGTTCTCATATGAGGCCATCATCACCCAC 1046
 Db 114483 ACGGCTCTCTGCATGGTCTCTCATCATGAGCCATCATCACCA 114542

Qy 1047 CTCTCATCTGTGATCCA 1063
 Db 114543 CTCTCATCTGTGATCCA 114559

RESULT 15

AC107608 AC107608 225030 bp DNA linear ROD 30-JUL-2003

DEFINITION Rattus norvegicus 1 BAC CH230-204P6 (Children's Hospital Oakland Research Institute) complete sequence.

ACCESSION AC107608

VERSION AC107608.6 GI:33342287

KEYWORDS HTG

Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Rattus norvegicus, Rattus rattus, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.

REFERENCE

1. (bases 1 to 225030)
 MUZZI,D., MARIE,M., METZKER,M., LEE,A., ABRAMSON,S., ADAMS,C., ALDER,J., ALLEN,C., ALLEN,H., ALSBROOKS,S., ANIN,A., ANGUILANO,D., ANYALABECHI,V., NOYADI,A., AYODEJI,M., BACA,E., BADEN,H., BALDWIN,D., BANDARANAIKE,D., BARBER,B., BARNETT,M., BENAHMED,F., BISWALO,K., BLAIR,J., BLANKENBURG,K., BLYTH,P., BROWN,M., BRYANT,N., BUNAY,C., BURCH,P., BURRELL,K., CALDERON,E., CARDENAS,V., CARTER,K., CAVAZOS,I., CEASER,H., CENTER,A., CHACKO,J., CHAVEZ,D., CHEN,G., CHEN,R., CHEN,Y., CHEN,Z., CHU,J.,

Cleveland,C., COCKRELL,R., COX,C., COYLE,M., CREE,A., D'SOUZA,L., DAVILA,M.L., DAVIS,C., DAVY-CARROLI,L., DE ANDA,C., DEDERICHS,D., DELGADO,O., DENISON,S., DERAMO,C., DING,Y., DINH,H., DIVYA,K., DRAPER,H., DUGAN-ROCHA,S., DUNN,A., DURBIN,B., DUVAL,B., EAVES,K., EGAN,A., ESCOTO,M., EUGENE,C., EVANS,C.A., FAILS,T., FAN,G., FERNANDEZ,S., FINLEY,M., FLIGG,N., FORBES,L., FOSTER,M., FOSTER,P., FRAZER,C.M., GABISI,A., GANIA,R., GARCIA,A., GARNER,T., GARZA,M., GEBREGEORGIS,E., GEER,K., GILL,R., GRADY,M., GUERRA,W., GHEVARA,W., GUNARATNE,P., HAALAND,W., HAMILT,C., HAMILTON,C., HERNANDEZ,K., HARVEY,Y., HAVLAK,P., HAWES,A., HENDERSON,N., HERNANDEZ,J., HERNANDEZ,R., HINES,S., HLADUN,S.L., HODGSON,A., HOGUES,M., HOLLINS,B., HOWELLS,S., HULYK,S., HUME,J., IALEBIRD,D., JACKSON,A., JACKSON,L., JACOB,L., JIANG,H., JOHNSON,B., JOHNSON,R., JOUVET,A., KARPATHY,S., KELLY,S., KELLY,S., KHAN,Z., KING,L., KOVAR,C., LIU,J., KOWIS,C., KRAFT,C.L., LEBOV,H., LEVAN,J., LEWIN,J., LI,J., LIU,J., LIU,J., LIU,W., LIU,Y., LONDON,P., LONGACRE,S., LOPEZ,J., LORENBUHWA,L., LOUISSEG,D., LUO,R.J., LU,X., MA,J., MAHESHWARI,M., MAHINDARINE,M., MAHMUD,M., MAILLY,K., MANGUM,A., MANGUM,B., MAPUA,P., MARTIN,K., MARTIN,R., MARTINEZ,B., MAWNINE,S., MCLEOD,M., MCNEIL,T., MEENE,E., MILESOVJLEVIC,A., MINER,G., MINJA,E., MONTEMAYOR,J., MOORE,S., MORGAN,M., MORRIS,K., MORRIS,S., MUNIDASA,M., MURPHY,M., NAIR,L., NANKERVIS,C., NEAL,D., NEWTON,N., NGUYEN,N., NORRIS,S., NWAOKELEMBH,O., OKWUNOU,G., OLARMPUNNAGOO,A., PAL,S., PARKS,K., PASTERNAK,S., PAUL,H., PEREZ,A., PEREZ,L., PFANNKUCH,C., PILOPER,F., POINDEXTER,A., POPOVIC,D., PRIMUS,E., PU,L.-L., PUZO,M., QUIROZ,J., RACHLIN,E., REEVES,K., REGIER,M.A., REIGN,R., REILLY,B., REILLY,M., REILLY,Y., REIFER,M., RICHARDS,S., RIGGS,F., RIVES,C., RODKEY,T., ROJAS,A., ROSE,M., ROSE,R., RUIZ,S.J., SANDERS,W., SAVERY,G., SCHERER,S., SCOTT,G., SHATSKIAN,S., SHEN,H., SHETTY,J., SHVARTSEBEIN,A., SIBSON,I., SISTER,C.D., SMALES,D., SNEED,A., SODEBERGEN,E., SONG,X.-Z., SORELLE,R., SOOL,J., STEINLE,M., STRONG,R., SUTTON,A., SVATEK,A., Tabor,P., TAYLOR,T., THOMAS,N., THOMAS,S., TINGEY,A., TREJOZ,Z., USMANI,K., VALAS,R., VERA,V., VILLASANA,D., WALDRON,L., WALKER,B., WANG,J., WANG,Q., WANG,S., WARREN,J., WARREN,R., WEIL,X., WHITE,F., WILLIAMS,G., WILSON,R., WLEZYK,R., WOODEN,H., WORLEY,K., WRIGHT,R., WU,J., YAKUB,S., YEN,J., YOUN,L., YOUN,V., YU,F., ZHANG,J., ZHOU,J., ZHOU,S., ZHAO,S., DUNN,D., VON NIEDERHAUSERN,A., WEISS,R., SMITH,D.R., HOLT,R.A., SMITH,H.O., WEINSTOCK,G., AND GIBBS,R.A.

REFERENCE

1. (bases 1 to 225030)
 WORLEY,K.C.

TITLE

Direct Submission

JOURNAL

Submitted (23-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE

2. (bases 1 to 225030)
 WORLEY,K.C.

AUTHORS

Direct Submission

JOURNAL

Submitted (19-NOV-2002) Human Genome Sequencing Consortium, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE

3. (bases 1 to 225030)
 WORLEY,K.C.

AUTHORS

Direct Submission

JOURNAL

Submitted (30-JUL-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT

On Jul 30, 2003 this sequence version replaced gi:25072936.

Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.

FEATURES

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Db 142982 ACGGCTCTCTGCTCATGGTTCTCTCATCATGGAGTCCATCATCACCTC 143041
OY 1047 CTCCATCATGTGATCCA 1063
Db 143042 CTCCTCATCTGATCCA 143058

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Job time : 5927.2 secs

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GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic Search, using sw model

Run on: September 30, 2004, 19:01:32 ; Search time 569,119 Seconds
 (without alignments)
 1164.646 Million cell updates/sec

Title: US-10-077-698-5
 Perfect score: 1560

Sequence: ttgcacagtcaggtaagc.....aaaaaaa 1560

Scoring table: OLIGO NUC Gap60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_29Jan04;*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001ab:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002s:*
- 7: geneseqn2003ab:*
- 8: geneseqn2003bs:*
- 9: geneseqn2003cb:*
- 10: geneseqn2004bs:*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1560	100.0	1550	3	Aaa64347
2	1560	100.0	1560	6	ABQ81227
3	1212	77.7	1561	3	Aaa49746
4	180	11.5	180	3	Aaa64344
5	138	8.8	138	3	Aaa64345
6	44	2.8	1056	6	ABP04869
7	44	2.8	1056	5	ABP73398
8	44	2.8	1086	6	ABP73399
9	44	2.8	1086	6	ABP73343
10	44	2.8	1086	7	ACG0998
11	44	2.8	1086	8	ABD7641
12	44	2.8	1160	7	ABX10627
13	44	2.8	1321	4	ADP08854
14	44	2.8	1458	4	AKL66039
15	44	2.8	1737	7	ABZ42599
16	44	2.8	1742	3	AAK49745
17	44	2.8	1743	3	AAK4346
18	44	2.8	1743	6	ABQ81226
19	42	2.7	933	9	ADL12755
20	40	2.6	1066	9	ADC7012
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22	40	2.6	3173	4	ACB82670
23	39	2.5	638	6	AAS62901

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28	38	2.4	489	8	ACT45264
29	38	2.4	490	8	ACT13024
30	38	2.4	500	5	ABY60845
31	38	2.4	517	8	ACT43949
32	38	2.4	762	5	AXM3995
33	38	2.4	768	6	ABU39413
34	38	2.4	813	2	AXX39904
35	38	2.4	912	5	ABT70564
36	38	2.4	919	3	AAC58786
37	38	2.4	930	7	ABT70067
38	38	2.4	1281	5	ADP52753
39	38	2.4	2631	5	ABE64404
40	38	2.4	29222	6	ABU39412
41	29	1.9	469	8	ACT45354
42	28	1.8	445	8	ACT44462
43	28	1.8	459	8	ACT28569
44	28	1.8	1291	3	AAC57666
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ALIGNMENTS

RESULT 1

ID: Aaa64347 standard; DNA, 1560 BP.
 ID: Aaa64347;
 AC: Aaa64347;

DT: 20-DEC-2000 (first entry)

XX DNA encoding a murine G-protein coupled receptor designated 14273.
 XX Mouse; G-protein coupled receptor; receptor-mediated disorder;
 KW 14273 :receptor; cardiovascular disease; congestive heart failure;
 KW cardiac myocyte hypertrophy; BB.

XX Mus sp.

XX Key location/Qualifiers
 FT 195..1280
 FT /*tag= a
 FT /product= "G-protein coupled receptor 14273"

FT WO20050596-A2.

XX WO20050596-A2.

XX 31-AUG-2000.

XX PD 28-FEB-2000; 2000WO-US005068.

PF PR 26-FEB-1999; 99US-00261599.

PR 08-DEC-1999; 99US-00456455.

XX (MILL-) MILLENIUM PHARM INC.

PA PI Glucksmann MA, Tsai F;

XX DR WPI: 2000-587184/55.

DR P-PSDB; AAB80539.

XX PT 14273 receptor polynucleotides and polypeptides, useful in the diagnosis

PT and treatment of receptor-mediated disorders such as cardiovascular disease.

XX P-PSDB; AAB80539.

XX Claim 3; Fig 7; 105pp; English.

XX CC The present sequence encodes a murine G-protein coupled receptor, designated 14273 receptor. The G-protein coupled receptor 14273 polypeptide is used to produce antibodies, in drug screening assays, and

Aa280388 Human col

Ach44239 Human fo

Ach44015 Human fo

Aco2281 Human sec

Ach45264 Human fo

Ach13024 Human adu

Abo60845 Human pro

Ach43949 Human fo

Ach39905 Gastric c

Aab52753 Human cod

Aab64404 DNA encod

Au139412 Human ele

Ach45354 Human fo

Ach34462 Human end

Ach28569 Human adu

Aab67666 Human sec

Abo81230 Mouse 142

CC to screen for agonist and antagonists. The antibodies are used for diagnostic applications, and to assess abnormal tissue distributions or abnormal expression during development. The antibodies are also useful for issue typing, and in forensic identification, as well as for inhibiting receptor function. The 14273 polymucleotides can be used to express the receptor, to detect genetic alterations in the 14273 gene, and as a source of primers and probes. The 14273 polymucleotides and polypeptides are also useful as a target for diagnosis and treatment of receptor-mediated disorders, especially cardiovascular diseases such as congestive heart failure caused by cardiac myocyte hypertrophy

XX Sequence 1560 BP; 321 A; 449 C; 390 G; 400 T; 0 U; 0 Other;

Query Match Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

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301 GGTGGTGTGAGGCTCTGGAGACCAACCGCTCTGGAGACTCTATTTGGTCACTGC 360

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421 GCTCTGGTCTCAACTCTCTGGCGGATTGCTCTCACAGGCCATCCCTAGTC 480

QY 481 TCGTGTGGCTGACTGAGGCCCTGGCTCTGGAGCCATTAGGATGTCGGTCACTTAATTT 540
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Db 781 TGGATGGCCAAACGGCATAGGAGAAATCTCATGGATGTTTGAGACTTGAAC 840
781 TGGATGGCCAAACGGCATAGGAGAAATCTCATGGATGTTTGAGACTTGAAC 840

QY 841 TCCCTGGTCCGGACTGTCATGTCAGTACTCCAAATTAGATCAGGAG 900
841 TCCCTGGTCCGGACTGTCATGTCAGTACTCCAAATTAGATCAGGAG 900

Db 901 CATCGCGGAAAGAGGCTTAGCTGAGCTACTCTGAGAGCCACAGATCGAGCT 960
901 CATCGCGGAAAGAGGCTTAGCTGAGCTACTCTGAGAGCCACAGATCGAGCT 960

Db 951 CCCAACAGACTACCGACTCTCGAGCTGAGCTCTCCCTCTCTCTCTCATCA 1020
951 CCCAACAGACTACCGACTCTCGAGCTGAGCTCTCCCTCTCTCTCATCA 1020

Db 1021 TGTGGAGTCCCATCATTCACCATCTTCACTTCACTTCAACTTCCGGCAGGCC 1080
1021 TGTGGAGTCCCATCATTCACCATCTTCACTTCACTTCAACTTCCGGCAGGCC 1080

Db 1081 TGGTCACTTGCCATCTCTTCTCTCTGGTCTGGCTTCACTTCAACTCTGCC 1140
1081 TGGTCACTTGCCATCTCTTCTCTCTGGTCTGGCTTCACTTCAACTCTGCC 1140

Db 1141 TAACCCATACTGTACACATCTGCTCTCTGGAGCTGAGGAGATTTTGCT 1200
1141 TAACCCATACTGTACACATCTGCTCTCTGGAGCTGAGGAGATTTTGCT 1200

Db 1141 TAAACCCATACTGTACACATCTGCTCTCTGGAGCTGAGGAGATTTTGCT 1200
1141 TAAACCCATACTGTACACATCTGCTCTCTGGAGCTGAGGAGATTTTGCT 1200

QY 1201 GCTCTTTTCCAGAGAGGGACATTACAGATACAGTCTGTCGGGAATGACT 1260
1201 GCTCTTTTCCAGAGAGGGACATTACAGATACAGTCTGTCGGGAATGACT 1260

Db 1261 TGTGTGTTTTCAGCTACTAGCTCTGGTCCAGGTGAACCAACGGGTGATGAA 1320
1261 TGTGTGTTTTCAGCTACTAGCTCTGGTCCAGGTGAACCAACGGGTGATGAA 1320

Db 1321 GGAGGTTTACTCTGAGGAAGGCCACCGTGGCCCTCTTAAATACCGACTCCA 1380
1321 GGAGGTTTACTCTGAGGAAGGCCACCGTGGCCCTCTTAAATACCGACTCCA 1380

QY 1381 ACACGAGCATCTACGGGCCAAATTAGGAATGTCGGTCACTTAATTT 1440
1381 ACACGAGCATCTACGGGCCAAATTAGGAATGTCGGTCACTTAATTT 1440

Db 1441 TCCCTAAAGAACCTCTCATGGTTCTTGTGACTCTTAACTGTTGTAATAT 1500
1441 TCCCTAAAGAACCTCTCATGGTTCTTGTGACTCTTAACTGTTGTAATAT 1500

Db 1501 GATCTAGTAAATTATTTATTAATGTTCTCTAACAAAAAAAAAAAAAA 1560
1501 GATCTAGTAAATTATTTATTAATGTTCTCTAACAAAAAAAAAAAAAA 1560

Db 1560 GATCTAGTAAATTATTTATTAATGTTCTCTAACAAAAAAAAAAAA 1560
1560 GATCTAGTAAATTATTTATTAATGTTCTCTAACAAAAAAAAAAAA 1560

RESULT 2

ID ABQ81227 standard; cDNA; 1560 BP.

ID ABQ81227

XX ABQ81227;

XX 05-DEC-2002 (first entry)

DE Mouse 14273 nucleic acid, associated with metabolic disorder.

KW Mouse; 14273; metabolic disorder; obesity; diabetes; anorexia; cachexia; anorectic; antidiabetic; anabolic; transgenic animal; gene therapy; gene; ss.

OS Mus musculus.

XH Key location/Qualifiers

PT 195..1280

FT /tag= a

FT /product= "14273"

XX WO200267868-A2.

XX

PD 06-SEP-2002.
 XX
 PP 26-FEB-2002; 2002NO-US006131.
 XX
 PR 26-FEB-2001; 2001US-0271655P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 PT Gimeno R, Tsai P;
 XX
 DR WPI: 2002-698629/75.
 DR PPSDB; ABB79907.
 XX
 PT Identifying a nucleic acid associated with a metabolic disorder, useful for diagnosing metabolic disorders, e.g. obesity, comprises contacting the sample with a probe comprising at least 25 contiguous nucleotides of the 14273 gene.
 XX
 PS Claim 1; Fig 2; 95pp; English.
 XX
 CC The present sequence is that of a murine nucleic acid, designated 14273, associated with metabolic disorders. 14273 molecules are expressed at high levels in adipose tissue, e.g. white adipose tissue and brown adipose tissue, as well as in pancreatic islets. They are upregulated during exposure to cold (i.e. under conditions that affect brown or white adipocyte metabolism) and downregulated in genetic models of obesity. 14273 knock-out mice, when fed a high-fat diet, gain more weight and have larger epididymal fat pads than wild-type mice. They also show increased levels of glucose and insulin upon fasting. A 14273 agonist may be beneficial to the treatment of obesity and/or type II diabetes by preventing fat accumulation on a high-fat diet and/or the increases in endogenous glucose production which occur in type II diabetes. The present invention provides 14273 nucleic acids, polypeptides and antibodies useful for the diagnosis and treatment of metabolic disorders including obesity, anorexia, cachexia and diabetes. Also provided are methods for identifying a subject having a metabolic disorder, for identifying a compound capable of modulating metabolic activity, methods for modulating metabolic activity or adipocyte activity (hyperplastic growth, hypertrophic growth or lipogenesis), methods for modulating lipogenesis or lipolysis in a subject, and a method for regulating endogenous glucose levels.
 XX
 SQ Sequence 1560 BP; 321 A; 449 C; 390 G; 400 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1560; DB 6; Length 1560;
 Best Local Similarity 100.0%; Prod. No. 0;
 Matches 1560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTGCGCAAGTCCTAGCGTAAGCCCTCTTCACTGCAATCTCACAGAAGGGGTCTCATGGAGTC 60
 DB 1 TTGCGCAAGTCCTAGCGTAAGCCCTCTTCACTGCAATCTCACAGAAGGGGTCTCATGGAGTC 60
 QY 61 TTAGCACACATCAGTGACACTTCCAGTGTCTGGCTTACCGAAATCTCACAGAAGGGGTCTCATGGAGTC 120
 DB 61 TTGACACATCAGTGACACTTCCAGTGTCTGGCTTACCGAAATCTCACAGAAGGGGTCTCATGGAGTC 120
 QY 121 TCGATGACCTCTTGACACGCCAGAGCGGCCAGCTGGCATCTCCGGAGCGCTG 180
 DB 121 TCGATGACCTCTTGACACGCCAGAGCGGCCAGCTGGCATCTCCGGAGCGCTG 180
 QY 181 GCCTGGCGCCGATGTCCTGAGTGTCTGGCATCTCCGGAGCGCTG 180
 DB 181 GCCTGGCGCCGATGTCCTGAGTGTCTGGCATCTCCGGAGCGCTG 180
 QY 241 CCTCTGGACCAAGTCATCCGACCCACTTCCTTCTTGAGGTCTAGGGACACC 300
 DB 241 CCTCTGGACCAAGTCATCCGACCCACTTCCTTCTTGAGGTCTAGGGACACC 300
 QY 301 GTTGTGGTGTGAGGTCTGGAGGACCGTCTGGACTCTCTTGGCTGTCACAGC 360
 DB 301 GTTGTGGTGTGAGGTCTGGAGGACCGTCTGGACTCTCTTGGCTGTCACAGC 360
 QY 361 TGGGCAACCTGTGCTCTAGTGCTGGTGGCCGGCTGGGGCGTCAGCCA 420

Db 361 TGGGCAACCTGTGCTCTAGTGCTGGTGGCCGGCTGGGGCGTCAGCCA 420
 QY 421 GCTCTGGCTCAACCTCTCTGCGCGGATTGGCTCTTCAACGGCACTCTAGTGCTGG 480
 Db 421 GCTCTGGCTCAACCTCTCTGCGCGGATTGGCTCTTCAACGGCACTCTAGTGCTGG 480
 QY 481 TCGTGTGGCTGACTAGGCGCTGGCTGGGGCGCTGCTGGCTGGCTGG 540
 Db 481 TCGTGTGGCTGACTAGGCGCTGCTGGCTGG 540
 QY 541 ACCTGATGACAATGAGCGCGAGGTAGAGTCTCACACTGSCCGCTGAGCTGG 600
 Db 541 ACCTGATGACAATGAGCGCGAGGTAGAGTCTCACACTGSCCGCTGAGCTGG 600
 QY 601 GCATGGTGTGACATGTGGCTGGCGCTGGCGGGCTGAGGCCCGCTGAGCTGG 660
 Db 601 GCATGGTGTGACATGTGGCTGGCGCTGGCGGGCTGAGGCCCGCTGAGCTGG 660
 QY 661 CGGACTCTGGCTTATGGGTTCTGGGTTCTGGGCTGGCGCGCTGCGCTTACACT 720
 Db 661 CGGACTCTGGCTTATGGGTTCTGGGCTGGCGCGCTGCGCTTACACT 720
 QY 721 TGTTCGGTGGCCGGCTCCGGCGCCGCTCCGGGGAGCAGGAATTCGATTGCACT 780
 Db 721 TGTTCGGTGGCCGGCTCCGGCGCCGCTCCGGGGAGCAGGAATTCGATTGCACT 780
 QY 781 TGGATGCGCCAACCGCATAGGAGAAATCTCATGGATGTGTGTTTGAGACTTGAACT 840
 Db 781 TGGATGCGCCAACCGCATAGGAGAAATCTCATGGATGTGTGTTTGAGACTTGAACT 840
 QY 841 TCCCTGGTGGCGGACTGCTGAGTGTGAGTACTCCAAATTAGATCGAGAAG 900
 Db 841 TCCCTGGTGGCGGACTGCTGAGTGTGAGTACTCCAAATTAGATCGAGAAG 900
 QY 901 CATCGCGAGAGGCTTACGTTAGCTGAGCTTGCTGAGTCTGAGTACTCGAGAGCT 960
 Db 901 CATCGCGAGAGGCTTACGTTAGCTGAGCTTGCTGAGTCTGAGTACTCGAGAGCT 960
 QY 961 CCCACACAGACTACGATCTCGAGAGCTTACGTTAGCTGAGTCTGAGTACTCGAGAGCT 1020
 Db 961 CCCACACAGACTACGATCTCGAGAGCTTACGTTAGCTGAGTCTGAGTACTCGAGAGCT 1020
 QY 1021 TGTGGAGTCCATCATCATACCATCTCTCTCATGTCACACTTCGGCAGAGCC 1080
 Db 1021 TGTGGAGTCCATCATCATACCATCTCTCTCATGTCACACTTCGGCAGAGCC 1080
 QY 1081 TGGTCACTTGGCATCCCTTCTCTCTCATCTCATCCAAACTTCGGCAGAGCC 1140
 Db 1081 TGGTCACTTGGCATCCCTTCTCTCTCATCTCATCCAAACTTCGGCAGAGCC 1140
 QY 1141 TAACCCCATACTGACATGTCGTTCTGGCTGGCTTCAAGTTCCAACTCTGCC 1200
 Db 1141 TAACCCCATACTGACATGTCGTTCTGGCTGGCTTCAAGTTCCAACTCTGCC 1200
 QY 1201 GCTCTTCTTCTGGAGGAGGCAATTACAGATAGCTGCTGGGAATGATCT 1260
 Db 1201 GCTCTTCTTCTGGAGGAGGCAATTACAGATAGCTGCTGGGAATGATCT 1260
 QY 1261 TGTCTGTATTCCAGGAAAGCCACCGTCTGGCTCCAGCTGACACCGCTGCTGAA 1320
 Db 1261 TGTCTGTATTCCAGGAAAGCCACCGTCTGGCTCCAGCTGACACCGCTGCTGAA 1320
 QY 1321 GGGAGTTACTTCAGGAAAGCCACCGTCTGGCTCCAGCTGACACCGCTGCTGAA 1380
 Db 1321 GGGAGTTACTTCAGGAAAGCCACCGTCTGGCTCCAGCTGACACCGCTGCTGAA 1380
 QY 1381 GGAGTTACTTCAGGAAAGCCACCGTCTGGCTCCAGCTGACACCGCTGCTGAA 1440
 Db 1381 ACACGAGGACATCTAGGGCGCCAAATTAGGATGTGCTGAGTAAATATT 1440
 QY 1441 TCCTTAAAGAACCTTCATGGTTCTTGTGACTTTTAAAGTGTGTTGAATAAT 1500

Db	1441 TCCCTAAAGACTCTCATGGTCTTGTGACTTTAGTGCTTGTATAT 1500
Oy	77.7%; Score 1212; DB 3; Length 1501
Qy	Best Local Similarity 99.7%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1462; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
Db	1 1501 GATCTAGTTATAATTATTAACGTGTCTACAAACAAAAAA 1560
R	RESULT 3
RAZ49746	RAZ49746 standard; cDNA; 1561 BP.
XX	XX
AC	AC
DT	DT
DE	Murine 14273 G-protein coupled receptor (GPCR) encoding cDNA.
XX	XX
G	G-protein coupled receptor; GPCR; 14273 receptor; mouse; somatostatin;
KW	KW cellular function/activity; galanin receptor; chemokine receptor; diagnosis; treatment; receptor-mediated disorder; screening; ss;
XX	XX
OS	OS Mus sp.
FH	Key
CDS	Location/Qualifiers
FT	195 . 1280
FT	/*tag= a
FT	/product= "Murine 14273 G-Protein coupled receptor"
FT	/note= "Ortholog of human 14273 GPCR"
FT	/transl_except= (pos:228..230, aa:Gly)
FT	/transl_except= (pos:15..317, aa:Val)
FT	/transl_except= (pos:1002..1004, aa:Ile)
FT	987..989 /*tag= b
FT	/note= "Encodes Thr"
XX	XX
PN	W020000611-A2.
XX	XX
PD	06-JAN-2000.
PP	99WO-US014842.
PR	30-JUN-1998; 99US-00107761.
PR	30-DEC-1998; 98US-00223538.
PR	26-FEB-1999; 99US-00261599.
XX	(MILL-) MILLENNIUM PHARM INC.
PA	Glucksmann Ma, Tsai F;
PT	DR
XX	WPI; 2000-147268/13.
DR	P-PSDB; AAY4663.
XX	XX
PT	Novel G-protein coupled receptor 14273 Polynucleotides and Polypeptides used as a target for diagnosis and treatment of receptor-mediated disorders.
PT	Claim 3a; Fig 7; 89pp; English.
PS	The present sequence is the cDNA encoding mouse G-protein coupled receptor (GPCR) 14273 protein, an ortholog of human 14273 GPCR. It is involved in modulation of a cellular function or activity upon binding of a ligand to the GPCR. The GPCR 14273 protein has homology to galanin receptor, chemokine receptor and somatostatin. GPCR 14273 sequences are useful as a target for diagnosis and treatment of receptor-mediated disorders. The polypeptide is used for screening of drugs, agonist, antagonists and to produce antibodies. The antibodies are used for diagnosis, to assess abnormal tissue distribution or expression during development, inhibiting receptor function, tissue typing and forensic identification. The DNA sequences are used to detect genetic alterations in the gene and as a source of primers and probes
XX	Sequence 1561 BP; 321 A; 453 C; 386 G; 400 T; 0 U; 1 Other;
Qy	Query
Db	Match
1	1 TTGCCAAGCTCAGCTAAGCTCTTCACATGCAATCTAGAAGGGTCTATGGAGTC
1	1 TTGCCAAGCTCAGCTAAGCTCTTCACATGCAATCTAGAAGGGTCTATGGAGTC
61	61 TTGACGCTACCTCTTGACAGCCACGCGCGACTCCGCATCTTGACGGAG
61	61 TTGACGCTACCTCTTGACAGCCACGCGCGACTCCGCATCTTGACGGAG
120	120 TTGATGACCTCTTGACAGCCACGCGCGACTCCGCATCTTGACGGAG
120	120 TTGATGACCTCTTGACAGCCACGCGCGACTCCGCATCTTGACGGAG
180	180 GCGCGGCGCCGGCGTGTCCCTGAAGTGACAGACAGAGGGCCCTGGCCCTGACA
180	180 GCGCGGCGCCGGCGTGTCCCTGAAGTGACAGACAGAGGGCCCTGGCCCTGACA
240	240 CCCTGACCGAAGTCAATGCAACGACCCACTTCCCTTCCTGCGATGTCAGGGGACACC
240	240 CCCTGACCGAAGTCAATGCAACGACCCACTTCCCTTCCTGCGATGTCAGGGGACACC
300	300 CCTGACCGAAGTCAATGCAACGACCCACTTCCCTTCCTGCGATGTCAGGGGACACC
300	300 CCTGACCGAAGTCAATGCAACGACCCACTTCCCTTCCTGCGATGTCAGGGGACACC
360	360 GGTGTTGTTGTTGAGCCCTGTCGGACTCTTCAGTCATCTTGTCCTACTGC
360	360 GGTGTTGTTGTTGAGCCCTGTCGGACTCTTCAGTCATCTTGTCCTACTGC
360	360 TGGGAACTGTGCTCTAGTGTGCTGGCGCGTGGCGCGTGGCGCGTGGCGTACGCA
360	360 TGGGAACTGTGCTCTAGTGTGCTGGCGCGTGGCGCGTGGCGCGTGGCGTACGCA
420	420 361 TGGGAACTGTGCTCTAGTGTGCTGGCGCGTGGCGCGTGGCGCGTGGCGTACGCA
420	420 361 TGGGAACTGTGCTCTAGTGTGCTGGCGCGTGGCGCGTGGCGCGTGGCGTACGCA
420	420 361 TGGGAACTGTGCTCTAGTGTGCTGGCGCGTGGCGCGTGGCGCGTGGCGTACGCA
420	420 361 TGGGAACTGTGCTCTAGTGTGCTGGCGCGTGGCGCGTGGCGCGTGGCGTACGCA
480	480 421 GCCTGGTGTCAACCTCTGCGGGATTTGCTCTAACAGCGCCATCCCTAGTGC
480	480 421 GCCTGGTGTCAACCTCTGCGGGATTTGCTCTAACAGCGCCATCCCTAGTGC
480	480 421 GCCTGGTGTCAACCTCTGCGGGATTTGCTCTAACAGCGCCATCCCTAGTGC
540	540 481 TCTGTGTGCGCTGGACTGTGAGGCCCTGCTGTTGGGGCCGTCCTCCACCTGCTCT
540	540 481 TCTGTGTGCGCTGGACTGTGAGGCCCTGCTGTTGGGGCCGTCCTCCACCTGCTCT
600	600 541 AGCTGTATGACATAGGGCGAGCGTCACATCTCACCTGCGCGTGGCGTACGCTGGAC
600	600 541 AGCTGTATGACATAGGGCGAGCGTCACATCTCACCTGCGCGTGGCGTACGCTGGAC
600	600 541 AGCTGTATGACATAGGGCGAGCGTCACATCTCACCTGCGCGTGGCGTACGCTGGAC
660	660 601 GCATGGTGTCCATCTGGCTCCGGCGCGCTGAGCCGGGGGGGGGGACTCAG
660	660 601 GCATGGTGTCCATCTGGCTCCGGCGCGCTGAGCCGGGGGGGGGGACTCAG
660	660 601 GCATGGTGTCCATCTGGCTCCGGCGCGCTGAGCCGGGGGGGGGGACTCAG
720	720 661 CGGCACTGCTGCTTCATGGGTTACTGGGCTCGGGCGCTGCCCTCTACCT
720	720 661 CGGCACTGCTGCTTCATGGGTTACTGGGCTCGGGCGCTGCCCTCTACCT
720	720 721 TGTTCGGCTGGCTGGCGACGGAAATTCGGTTTGACAT
720	720 721 TGTTCGGCTGGCTGGCGACGGAAATTCGGTTTGACAT
780	780 781 TGGATGGCCAAAGCATAGGAAATCTATGGATGTTTGACCTTGACT
780	780 781 TGGATGGCCAAAGCATAGGAAATCTATGGATGTTTGACCTTGACT
840	840 841 TCTGTGTGCGGGACTGTGATGATGATGATGTTTGACCTTGACT
840	840 841 TCTGTGTGCGGGACTGTGATGATGATGATGTTTGACCTTGACT
900	900 901 CATCCGGAAAGGGTTAGCTGACTTCGACTTCGACTTCGAGAGGCCACAGATCCGGATG
900	900 901 CATCCGGAAAGGGTTAGCTGACTTCGACTTCGACTTCGAGAGGCCACAGATCCGGATG
960	960 901 CATCCGGAAAGGGTTAGCTGACTTCGACTTCGACTTCGAGAGGCCACAGATCCGGATG
960	960 961 CCCACAAAGCTACGACTCTCCACCTCTCTCTGATGTTCTCTCATCA
960	960 961 CCCACAAAGCTACGACTCTCCACCTCTGATGTTCTCTCATCA

Db 1021 TGGAGAGCCATCATCACACCACTCCTCATTCATCACAATTCGGCGAGGCC 1080
 OY 1081 TGGTCATCTGGCCATCCCTTCTCTGGGGGCGCTTCACCTTGCC 1140
 Db 1081 TGGTCATCTGGCCATCCCTTCTCTGGGGGCGCTTCACCTTGCC 1140
 CC to detect genetic alterations in the 14273 gene, and as a source of
 polymucleotides can be used to express the protein, to detect 14273 mRNA,
 primers and probes. The 14273 polymucleotides and polypeptides are also
 useful as a target for diagnosis and treatment of receptor-mediated
 disorders, especially cardiovascular diseases such as congestive heart
 failure caused by cardiac myocyte hypertrophy

SQ Sequence 180 BP; 37 A; 54 C; 36 G; 53 T; 0 U; 0 Other;

Query Match 11.5%; Score 180; DB 3; Length 180;
 Best Local Similarity 100.0%; Pred. No. 2e-63; P.
 Matches 180; Conservative 0; Mismatches 0; Indels 0; GapB 0;

OY 1021 TGGAGAGCCATCATCACACCACTCCTCTGGCTTCACCTTGCC 1080
 Db 1 1 TGGAGAGCCATCATCACACCACTCCTCTGGCTTCACCTTGCC 60
 OY 1081 TGGTCATCTGGCCATCCCTTCTCTGGGGGCGCTTCACCTTGCC 1140
 Db 61 1 TGGTCATCTGGCCATCCCTTCTCTGGGGGCGCTTCACCTTGCC 120
 OY 1141 TAACCCCCATACTGACACATGCTGAGGATGATGCGTCAAGTATAAATT 1440
 Db 1381 ACACAGGGCATACAGGAGCCAAATTAGGERATGATGCTCAGTATAAATT 1440
 OY 1441 TCCTTAAGAACGCTTCTATGGTCC 1467
 Db 1441 TCCCTTAAGAACGACTTCTATGGTCC 1467

RESULT 4
 AAA6434 standard; DNA; 180 BP.

ID AAA6434
 XX
 AC AAA6434;
 XX
 DT 20-DEC-2000 (first entry)

DE Probe for murine G-protein coupled receptor designated cDNA.

XX Human; G-protein coupled receptor; receptor-mediated disorder; 14273 receptor; cardiovascular disease; congestive heart failure; cardiac myocyte hypertrophy; probe; ss.

XX Homo sapiens.

OS Homo sapiens.

XX WO2000050596-A2.

PN WO2000050596-A2.

PD 31-AUG-2000.

XX
 PR 28-FEB-2000; 2000WO-US005068.

XX 26-FEB-1999; 99US-00261539.
 PR 08-DEC-1999; 99US-00456455.

XX (MILL-) MILLENIUM PHARM INC.

PT Glucksmann MA, Tsai P;
 XX DR WPI; 2000-587184/55.

XX
 PR 14273 receptor polynucleotides and polypeptides, useful in the diagnosis
 PT and treatment of receptor-mediated disorders such as cardiovascular
 diseases.

XX Example 2; Page 77; 105pp; English.

XX The present sequence represents a probe for cDNA encoding a murine G-
 CC protein coupled receptor designated 14273 receptor. The G-protein
 CC coupled receptor 14273 polypeptide is used to produce antibodies, in drug
 screening assays, and to screen for agonist and antagonists. The
 CC antibodies are used for diagnostic applications, and to assess abnormal
 tissue distributions or abnormal expression during development. The
 CC antibodies are also useful for tissue typing, and in forensic
 identification, as well as for inhibiting receptor function. The 14273
 polymucleotides can be used to express the protein, to detect 14273 mRNA,
 primers and probes. The 14273 polymucleotides and polypeptides are also
 useful as a target for diagnosis and treatment of receptor-mediated
 disorders, especially cardiovascular diseases such as congestive heart
 failure caused by cardiac myocyte hypertrophy

SQ Sequence 180 BP; 37 A; 54 C; 36 G; 53 T; 0 U; 0 Other;

Query Match 11.5%; Score 180; DB 3; Length 180;
 Best Local Similarity 100.0%; Pred. No. 2e-63; P.
 Matches 180; Conservative 0; Mismatches 0; Indels 0; GapB 0;

OY 1021 TGGAGAGCCATCATCACACCACTCCTCTGGCTTCACCTTGCC 1080
 Db 1 1 TGGAGAGCCATCATCACACCACTCCTCTGGCTTCACCTTGCC 60
 OY 1081 TGGTCATCTGGCCATCCCTTCTCTGGGGGCGCTTCACCTTGCC 1140
 Db 61 1 TGGTCATCTGGCCATCCCTTCTCTGGGGGCGCTTCACCTTGCC 120
 OY 1141 TAACCCCCATACTGACACATGCTGAGGATGATGCGTCAAGTATAAATT 1440
 Db 121 TAACCCCCATACTGACACATGCTGCTGTTAGGAAGGAATGAGATTTCCT 180

RESULT 5
 AAA64345 standard; DNA; 138 BP.

ID AAA64345
 XX
 AC AAA64345;
 XX
 DT 20-DEC-2000 (first entry)

DE Probe for murine G-protein coupled receptor designated cDNA.

XX Human; G-protein coupled receptor; receptor-mediated disorder; 14273 receptor; cardiovascular disease; congestive heart failure; cardiac myocyte hypertrophy; probe; ss.

XX Homo sapiens.

OS Homo sapiens.

PN WO2000050596-A2.

XX
 PD 31-AUG-2000.

XX
 PR 28-FEB-2000; 2000WO-US005068.

XX 26-FEB-1999; 99US-00261539.
 PR 08-DEC-1999; 99US-00456455.

XX (MILL-) MILLENIUM PHARM INC.

PT Glucksmann MA, Tsai P;
 XX DR WPI; 2000-587184/55.

XX
 PR 14273 receptor polynucleotides and polypeptides, useful in the diagnosis
 PT and treatment of receptor-mediated disorders such as cardiovascular
 diseases.

XX Example 2; Page 77; 105pp; English.

XX The present sequence represents a probe for cDNA encoding a murine G-
 CC protein coupled receptor designated 14273 receptor. The G-protein
 CC coupled receptor 14273 polypeptide is used to produce antibodies, in drug
 screening assays, and to screen for agonist and antagonists. The
 CC antibodies are used for diagnostic applications, and to assess abnormal
 tissue distributions or abnormal expression during development. The

CC antibodies are also useful for tissue typing, and in forensic identification, as well as for inhibiting receptor function. The 14273 mRNAs are useful for expressing the protein, to detect 14273 genetic alterations in the 14273 gene, and as a source of primers and probes. The 14273 polymucleotides and polypeptides are also useful as a target for diagnosis and treatment of receptor-mediated disorders, especially cardiovascular diseases such as congestive heart failure caused by cardiac myocyte hypertrophy

CC Sequence 138 BP; 30 A; 46 C; 26 G; 36 T; 0 U; 0 Other;

CC Query Match 8.8%; Score 138; DB 3; Length 138;

CC Best Local Similarity 100.0%; Pred. No. 2.8e-46;

CC Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 909 AAGAGGCTTACGCTTGAAGCTGCATACTCTGGAGGCCACAGATCCGGAGTGTCCACAA

DB 1 AAGAGGCTTACGCTTGAAGCTGCATACTCTGGAGGCCACAGATCCGGAGTGTCCACAA

OY 969 GACGACCGACTCTTGACGCTCTTCCTGCTCATGTTCTCTTCATCATTGAGT

DB 61 GACTAACGACTCTTCGACGCTCTTCGTCAGCGCTCTCTGCTCATGGTTCTCTTCATCATTGAGT

OY 1029 CCCATCATCATCACCATC 1046

DB 121 CCCATCATCATCACCATC 138

RESULT 6

ID ABT04869

ID ABT04869 standard; cDNA; 1086 BP.

XX AC

XX AC

XX DT 11-OCT-2002 (first entry)

XX DE Human G protein coupled receptor hrUP31 coding sequence.

XX KW Human; G-protein coupled receptor; GPCR; hrUP28; hrUP29; hrUP30; hrUP31; hrUP32; hrUP33; hrUP34; hrUP35; hrUP36; hrUP37; gene; ss.

XX OS Homo sapiens.

XX PN WO200242461-A2.

XX PD 30-MAY-2002.

XX PF 26-NOV-2001; 2001WO-US044386.

PR 27-NOV-2000; 2000US-0253404P.

PR 12-DEC-2000; 2000US-0253366P.

PR 20-FEB-2001; 2001US-0271266P.

PR 20-FEB-2001; 2001US-0270286P.

PR 06-APR-2001; 2001US-028032P.

PR 06-APR-2001; 2001US-0282356P.

PR 06-APR-2001; 2001US-0282358P.

PR 06-APR-2001; 2001US-0283365P.

PR 14-MAY-2001; 2001US-0290917P.

PR 31-JUL-2001; 2001US-030208P.

XX PA (AREN-) ARENA PHARM INC.

XX PI Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;

XX DR WPI; 2002-565565/60.

XX DR P-FSDB; ABJ04071.

PT Novel endogenous and non-endogenous versions of G protein-coupled receptor useful for identification of candidate compounds as receptor agonists or antagonists for use as therapeutic agents.

PT Claim 15; Page 61; 84pp; English.

The present invention provides the protein and coding sequences of several human G-protein coupled receptors (GPCRs). These can be used in the identification of candidate compounds as receptor agonists or inverse agonists having applicability as therapeutic agents. The present sequence is a GPCR coding sequence of the invention.

XX	KW	nootropic; neuroprotective; antiparkinsonian; antidiabetic;
XX	KW	anti-depressant; hypotensive; tranquilizer; nephrotoxic;
XX	KW	cell growth disorder; neurological condition; pituitary gland disorder;
XX	KW	colon disorder; breast disorder; lung disorder; prostate disorder;
XX	KW	Alzheimer's disease; Parkinson's disease; diabetes; dwarfism;
XX	KW	colour blindness; retinal pigmento; asthma; depression; schizophrenia;
XX	KW	sleeplessness; hypertension; anxiety; stress; renal failure; gene; ss.
OS	KW	
XX	KW	Homo sapiens.
Key	Location/Qualifiers	
FT	CDS	
FT	1. .1083	
FT	/*tag= a	
FT	/product= "HGPBMY18"	
FT	/note= "Human G protein coupled receptor"	
XX	US2003022186-A1.	
PN	PA	14-NOV-2001; 2001US-0092331.
XX	PA	14-NOV-2001; 2000US-024483P.
PR	PA	16-JAN-2001; 2001US-0261782P.
PR	PA	27-JUL-2001; 2001US-0308540P.
XX	(FEDER/) FEDER J N.	
PA	(MINT/) MINTIER G.	
PA	(RAMA/) RAMANATHAN C S.	
PT	Pedar JN, Mintier G, Ramanathan CS;	
XX	DR	WPI: 2003-416985/39.
DR	P-PSDB; ABU09715.	
XX	PT	New isolated human GPCR, HGPBMY18, polynucleotide and polypeptide, useful for treating, diagnosing and preventing disorders such as cancer, neurological conditions, and diseases of the pituitary gland, colon, breast and lungs.
XX	PT	Claim 1; Fig 1; 66pp; English.
PS	CC	The invention describes a new isolated polynucleotide encoding a human G-protein coupled receptor (GPCR) or its functional fragment. The methods and compositions of the present invention are useful for treating, diagnosing, preventing and screening disorders associated with aberrant pituitary gland, colon, breast, lungs, and prostate. These disorders include Alzheimer's, Parkinson, diabetes, dwarfism, colour blindness, retinal pigmentosa, asthma, depression, schizophrenia, sleeplessness, hypertension, anxiety, stress and renal failure. This sequence encodes novel human G protein coupled receptor HGPBMY18
SQ	XX	Sequence 1086 BP; 182 A; 349 C; 295 G; 260 T; 0 U; 0 Other; 2.8%; Score 44; DB 7; Length 1086; Best Local Similarity 100.0%; Pred. No. 4.6e-08; Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	CC	Query Match 852 GGACTGGTCATGGTACAGTACTCCAAATTACAGATCAC 895 Db 658 GGACTGGTCATGGTACAGTACTCCAAATTACAGATCAC 701
RESULT 11	XX	
ID	AC	ADB47641 standard; cDNA; 1086 BP.
ID	AC	ADB47641;
DT	04-DEC-2003 (first entry)	
XX	XX	Human cDNA encoding GPCR, HGPBMY18.

CC aberrant testosterone synthesis and/or secretion, aberrant oestrogen
 CC synthesis and/or secretion, aberrant water homeostasis, hypogonadism,
 CC Addison's disease, hypothyroidism, Cushing's disease, agromegaly, aberrant
 CC potassium homeostasis, reproductive disorders, developmental disorders,
 CC colon cancer, related proliferative condition of the colon, breast
 CC cancer, related proliferative condition of the breast, prostate cancer,
 CC proliferative condition of the lung. In addition determining the presence
 CC or amount of expression of HGPRTM18 is useful for diagnosing a
 CC (susceptibility to a) pathological condition such as colon cancer,
 CC related proliferative condition of the colon, breast cancer, related
 CC proliferative condition of the breast, prostate cancer, related
 CC proliferative condition of the prostate, lung cancer, and related
 CC HGPRTM18.

SO Sequence 1086 BP; 182 A; 349 C; 295 G; 260 T; 0 U; 0 Other;

Query Match 2.8%; Score 44; DB 8; Length 1086;
 Best Local Similarity 100.0%; Pred. No. 4 6e-08; Mismatches 0; Indels 0; Gaps 0;
 Matches 44; Conservative 0;

Ov 852 GGACTGGCATATGATCTGATCTACTCCAAATTACAGATAC 895
 Db 658 GGACTGGCATATGATCTACTCCAAATTACAGATAC 701

RESULT 12

ABX10327
 ID ABX10627 standard; DNA; 1160 BP.

AC ABX10327;
 XX
 AC ABX10627;

DE DNA encoding human orphan SNORF49 receptor.

XX Human; gene; ds; SNORF49 receptor; neuroregulator; inflammation;

KW arthritis; autoimmune disease; transplant rejection; infection;

KW septicaemia; AIDS; neurological disorder; schizophrenia; epilepsy;

KW respiratory disorder; asthma; obesity; diabetes; anorexia;

KW cardiovascular disorder; ischaemia; stroke; cancer; sexual/reproductive

KW reproductive disorder; circadian rhythm disorder; renal disorder;

KW bone disease; osteoporosis; allergy; Parkinson's disease;

KW Alzheimer's disease.

OS Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 28..1113
 FT /*tag= a
 FT /product= "SNORF49 receptor"

PN US2002151705-A1.

PD 17-OCT-2002.

PP 11-DEC-2001; 2001US-00015498.

PR 05-OCT-1999; 99US-00412933.

XX PA (SMITH/) SMITH K. E.
 PA (QUAN/) QUAN Y.

PT Smith KE, Quan Y;

XX DR WPI; 2003-198336/19.

DR P-PSDB; AB373199.

XX New recombinant nucleic acid comprising a nucleic acid encoding a
 PT mammalian SNORF49 receptor, useful for screening antagonist to the
 PT SNORF49 receptor or as probes to obtain homologous nucleic acids from

PT other species.

XX Claim 2; Fig 1; 13pp; English.

CC The invention discloses a recombinant nucleic acid comprising a nucleic
 CC acid encoding a mammalian SNORF49 receptor, having a sequence identical
 CC to the sequence of the human SNORF49 receptor-encoding nucleic acid
 CC contained in plasmid PBXJ-T73BS-HS-SNORF49-f. SNORF49 receptor is a
 CC neuromodulator. The nucleic acid is useful for expressing the receptor in
 CC transfected cells, for screening for antagonists to the SNORF49 receptor
 CC or as probes to obtain homologous nucleic acids from other species and to
 CC detect the existence of nucleic acids having complementary sequences in
 CC samples. The receptor can also be used in the design of drugs for
 CC treating various pathophysiological conditions such as inflammation,
 CC arthritis, autoimmune disease, transplant rejection, infections,
 CC septicemia, AIDS, neurological disorders, such as schizophrenia and
 CC epilepsy, respiratory disorders, asthma, obesity, diabetes, anorexia,
 CC cardiovascular disorders, ischaemia, stroke, cancer, sexual/reproductive
 CC disorders, circadian rhythm disorder, renal disorders, bone diseases,
 CC osteoporosis, allergy, Parkinson's disease and Alzheimer's disease. The
 XX sequence presented is the DNA encoding the human orphan SNORF49 receptor

SO Sequence 1160 BP; 192 A; 372 C; 318 G; 278 T; 0 U; 0 Other;

Query Match 2.8%; Score 44; DB 7; Length 1160;

Best Local Similarity 100.0%; Pred. No. 4 6e-08; Mismatches 0; Indels 0; Gaps 0;

Matches 44; Conservative 0;

Ov 852 GGACTGGCATATGATCTACTCCAAATTACAGATAC 895
 Db 685 GGACTGGCATATGATCTACTCCAAATTACAGATAC 728

RESULT 13

AAD08854
 ID AAD08854 standard; cDNA; 1321 BP.

AC AAD08854;

XX DT 04-SEP-2001 (first entry)

XX DE Human G-protein coupled receptor-20 (GCRC-20) cDNA.

XX Human; G-protein coupled receptor-20; GCRC-20; gene therapy; cirrhosis;

XX transgenic animal; proliferative disorder; actinic keratosis;

XX hepatitis; nephrotoxic; cancer; breast; bladder; bone marrow; brain;

XX uterus; leukaemia; adenocarcinoma; lymphoma; melanoma; myeloma; epilepsy;

XX stroke; neurologic disorder; Alzheimer's disease; Parkinson's disease;

XX nausea; Huntington's disease; multiple sclerosis; dementia;

XX angina pectoris; central nervous system disorder;

XX cardiovascular disorder; hypertension; atherosclerosis;

XX congestive heart failure; gastrointestinal disorder; dysphagia;

XX peptic oesophagitis; spasm; gastritis; anorexia; pyrosis; pancreatitis;

XX Crohn's disease; diarrhoea; autoimmune disorder; anaemia;

XX inflammatory disorder; Acquired Immune Deficiency Syndrome; AIDS;

XX Addison's disease; allergy; asthma; diabetes mellitus; antithyroid;

XX atopic dermatitis; glomerulonephritis; Grav's disease; psoriasis;

XX rheumatoid arthritis; ulcerative colitis; osteoporosis; anti-tumour;

XX metabolic disorder; obesity; motropic; protozoacide; virucide; ss;

OS Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 30..1115
 FT /*tag= a
 FT /product= "Human GCRBC-20 protein"

PN WO200142288-A2.

XX PD 14-JUN-2001.

XX PP 07-DEC-2000; 2000WO-US033182.

XX

PR 10-DEC-1999; 99US-0172853P.
 PR 22-DEC-1999; 99US-0171732P.

PR 14-JAN-2000; 2000US-0176148P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.

XX Burford N, Baughn MR, Au-Young J, Yang J, Lu DAM, Reddy R;
 XX DR WPI; 2001-381635/40.
 XX DR p-PSDB; AAE04564.

XX PT New human G-protein coupled receptor polypeptides for diagnosing,
 PT preventing, and treating cell proliferative, neurological, autoimmune and metabolic disorders.

XX PS Claim 5; Page 167; 175pp; English.

XX The present sequence is human G-protein coupled receptor-20 (GCREC-20)
 CC GCREC is useful in somatic or germline gene therapy to correct a
 CC genetic deficiency, to express a conditionally lethal gene product and to
 CC express a protein which affords protection against intracellular
 CC parasites and also for diagnosis of disorders associated with expression
 CC of GCREC. GCREC is also useful for generating hybridisation probes useful
 in mapping the naturally occurring genomic sequences and to create
 CC knockin humanised animals (pigs) or transgenic animals (mice or rats) to
 CC model human diseases. GCREC is used to diagnose, prevent and treat
 CC proliferative disorders (actinic keratosis, arteriosclerosis, cirrhosis,
 CC hepatitis and cancer); cancer (breast, bladder, bone marrow, brain, melanoma and myeloma)
 CC neurological disorders (epilepsy, stroke, Alzheimer's, Huntington's,
 CC Parkinson's disease, multiple sclerosis, dementia and other central
 CC nervous system disorders); cardiovascular disorders (angina pectoris,
 CC hypertension, atherosclerosis, congestive heart failure);
 CC gastrointestinal disorders (dysphagia, peptic oesophagitis, oesophageal
 CC spasm, gastritis, gastric carcinoma, anorexia, nausea, abdominal angina,
 CC pyrosis, pancreatitis, Crohn's disease, diarrhoea); autoimmune/
 CC inflammatory disorders (acquired immunodeficiency syndrome (AIDS),
 CC Addison's disease, allergies, anaemia, asthma, diabetes mellitus, atopic
 CC dermatitis, glomerulonephritis, Grave's disease, osteoarthritis,
 CC psoriasis, rheumatoid arthritis, ulcerative colitis, bacterial, fungal,
 CC parasitic, protozoal and helminthic infections) and metabolic disorders
 CC (obesity, osteoporosis, viral infections)

XX Sequence 1321 BP; 243 A; 404 C; 348 G; 326 T; 0 U; 0 Other;

XX Query Match 2.8%; Score 44; DB 4; Length 1458;

CC Best Local Similarity 100.0%; Pred. No. 4.5e-08;

CC Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC SQ Sequence 1458 BP; 271 A; 445 C; 386 G; 356 T; 0 U; 0 Other;

CC ID AB242599 standard; DNA; 1737 BP.

XX AC AB242599;

XX DT 04-MAR-2003 (first entry)

XX DE Human G protein-coupled receptor 14273 nucleotide SEQ ID NO:681.

XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;

XX KW G protein-coupled receptor modulator; antibody; immune-related disease;

XX KW growth-related disease; cell regeneration-related disease; AIDS; cancer;

XX KW immunological-related disease; autoimmune disease; allergy;

XX KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;

XX KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;

XX KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;

XX KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;

XX KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;

XX KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;

XX KW ulcer; gene; ds.

XX OS Homo sapiens.

XX PN WO200261087-A2.

XX DT 08-AUG-2002 (first entry)

XX DE Human G protein-coupled receptor encoding cDNA SEQ ID NO 2.

XX KW Human; G protein-coupled receptor; cytostatic; cancer; hypophyphysisim;

XX KW ssb.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT 58..1143

FT /product= "G protein-coupled receptor"
 FT /note= "claimed in claim 6"

FT JP2001211885-A.

FT 02-FEB-2000; 2000JP-00024921.

FT 02-FEB-2000; 2000JP-00024921.

FT (KYO) KYOWA HAKKO KOGYO KK.

FT DR WPI; 2001-629567/73.

FT DR p-PSDB; AAM51426.

FT A new G protein-coupled receptor polypeptide.

FT PS Claim 6; Page 41-42; 52pp; Japanese.

FT The invention relates to a human G protein-coupled receptor polypeptide

CC with cytostatic activity and used for the treatment of cancers or

CC hypophysism

XX SQ Sequence 1458 BP; 271 A; 445 C; 386 G; 356 T; 0 U; 0 Other;

CC ID AB242599 standard; DNA; 1737 BP.

XX AC AB242599;

XX DT 04-MAR-2003 (first entry)

XX DE Human G protein-coupled receptor 14273 nucleotide SEQ ID NO:681.

XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;

XX KW G protein-coupled receptor modulator; antibody; immune-related disease;

XX KW growth-related disease; cell regeneration-related disease; AIDS; cancer;

XX KW immunological-related disease; autoimmune disease; allergy;

XX KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;

XX KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;

XX KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;

XX KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;

XX KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;

XX KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;

XX KW ulcer; gene; ds.

XX OS Homo sapiens.

XX PN WO200261087-A2.

XX DT 08-AUG-2002.

XX DE 19-DEC-2001; 2001WO-US050107.

XX KW (LIFE-) LIFESPAN BIOSCIENCES INC.

XX PI Burmer GC, Roush CL, Brown JP;

XX DR WPI; 2003-046718/04.

XX DR p-PSDB; ABP81754.

Fri Oct 1 07:43:11 2004

XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.
XX
PS Disclosure; Fig 1; 523pp; English.

XX
CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP8219 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample,
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological related cell proliferative
CC disease, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ4523 to ABZ42859 encode
CC GPCR proteins given in ABP81675 to ABP8218, which are used in the
CC exemplification of the present invention
XX

SQ Sequence 1737 BP; 377 A; 487 C; 440 G; 430 T; 0 U; 3 Other;

Query Match 2.8%; Score 44; DB 7; Length 1737;
Best Local Similarity 100.0%; Pred. No. 4.4e-08;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 852 GAGCTGGCATCTGATCAGTACTCCAAATTACAGATAC 895
Db 701 GAGCTGGCATCTGATCAGTACTCCAAATTACAGATAC 744

Search completed: September 30, 2004, 22:12:48
Job time : 572.119 secs

OM nucleic - nucleic search, using BW model
 Run on: September 30, 2004, 21:52:37 ; Search time 731.589 Seconds
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RESULT 1
US-10-086-181-4

; Sequence 4, Application US/0086181
; Publication No. US2002017715A1

; GENERAL INFORMATION:

; APPLICANT: GIMENO, Ruth

; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF METABOLIC DISORDERS, INCLUDING OBESITY AND DIABETES

; FILE REFERENCE: WOI-220

; CURRENT APPLICATION NUMBER: US/10/086,181

; CURRENT FILING DATE: 2002-02-26

; PRIOR APPLICATION NUMBER: 60/271,655

; PRIOR FILING DATE: 2001-02-26

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 1560

; TYPE: DNA

; ORGANISM: Murine ortholog

; FEATURE: CDS

; NAME/KEY: (195) ... (1280)

; LOCATION: US-10-086-181-4

Query Match 100.0%; Score 1560; DB 14; Length 1560;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1560; Conservative 0; Misnmatches 0;

Qy 1 TGGCAAGCTCGGTAGGCTTCACTGCAATCTCACAGCGAGCTGGCAACTTCCGGACGGCTG 120
Db 1 TTGCCAAGCTCGGTAGGCTTCACTGCAATCTCACAGAGGCTCATGGAGTC 60
Qy 61 TTGACACCATCAGTGGACCACTCCAGACTGTCGGCTTACCGAATCTCACAGCGAG 120
Db 61 TTGACACCATCAGTGGACCACTCCAGACTGTCGGCTTACCGAATCTCACAGCGAG 120
Qy 121 TGATGACCCCTTGAGCAGGCCAGAGGGGGCAGCTGGCAACTTCCGGACGGCTG 180

ALIGNMENTS

Sequence 1, Appl
Sequence 7, Appl
Sequence 3, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 78, Appl
Sequence 80, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 1895, AP
Sequence 1809, AP
Sequence 1, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 5, Appl
Sequence 58, Appl
Sequence 1916, AP
Sequence 1915, AP
Sequence 1919, AP
Sequence 472, AP
Sequence 1923, AP
Sequence 1921, AP
Sequence 1926, AP
Sequence 1913, AP
Sequence 1910, AP
Sequence 1925, AP

US-10-086-181-6

Query Match 69.4% Score 1086; DB 14; Length 1086;
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 1086; Conservative 0;

QY 781 TGGATTGGCCCAACCGCATAGAGAAATCTCATGGATGTGTTTGGACATTGA 840
 Db 781 TGGATTGGCCCAACCGCATAGAGAAATCTCATGGATGTGTTTGGACATTGA 840

QY 841 TCTTGTTGGGGACTGGTCATIGTCACTGAAATTAGATGAGGAGA 900
 Db 841 TCTTGTTGGGGACTGGTCATIGTCACTGAAATTAGATGAGGAGA 900

QY 901 CATGCGGAAGAGCTTACGGTAGCTGGACACTCTGAGGCCACAGATCGAGT 960
 Db 901 CATGCGGAAGAGCTTACGGTAGCTGGACACTCTGAGGCCACAGATCGAGT 960

QY 960 CATCGGGAGAGCTTACGGTAGCTGGACACTCTGAGGCCACAGATCGAGT 960
 Db 960 CATCGGGAGAGCTTACGGTAGCTGGACACTCTGAGGCCACAGATCGAGT 960

QY 1021 TGGGAGTCCCACATCATGGCTTCTCTCTGGGGTGGCTTCACCTGCGCC 1080
 Db 1021 TGGGAGTCCCACATCATGGCTTCTCTCTGGGGTGGCTTCACCTGCGCC 1080

QY 1080 TGGGAGTCCCACATCATGGCTTCTCTCTGGGGTGGCTTCACCTGCGCC 1080
 Db 1080 TGGGAGTCCCACATCATGGCTTCTCTCTGGGGTGGCTTCACCTGCGCC 1080

QY 1140 TGGGAGTCCCACATCATGGCTTCTCTCTGGGGTGGCTTCACCTGCGCC 1140
 Db 1140 TGGGAGTCCCACATCATGGCTTCTCTCTGGGGTGGCTTCACCTGCGCC 1140

QY 1141 TAACCCCATACATCTGAGATGAGGATTTCTGAGATGAGTGTGCTTCAC 1200
 Db 1141 TAACCCCATACATCTGAGATGAGGATTTCTGAGATGAGTGTGCTTCAC 1200

QY 1200 TAACCCCATACATCTGAGATGAGGATTTCTGAGATGAGTGTGCTTCAC 1200
 Db 1200 TAACCCCATACATCTGAGATGAGGATTTCTGAGATGAGTGTGCTTCAC 1200

QY 1260 TGGCTGTTTCCAGAGAGGACCTTACAGATGAGTGTGCTTCAC 1260
 Db 1260 TGGCTGTTTCCAGAGAGGACCTTACAGATGAGTGTGCTTCAC 1260

QY 1320 TGGCTGTTTCCAGAGAGGACCTTACAGATGAGTGTGCTTCAC 1320
 Db 1320 TGGCTGTTTCCAGAGAGGACCTTACAGATGAGTGTGCTTCAC 1320

QY 1380 AGCGAGGAGCTTACAGATGAGTGTGCTTCAC 1380
 Db 1380 AGCGAGGAGCTTACAGATGAGTGTGCTTCAC 1380

QY 1380 AGCGAGGAGCTTACAGATGAGTGTGCTTCAC 1380
 Db 1380 AGCGAGGAGCTTACAGATGAGTGTGCTTCAC 1380

QY 1440 AGCGAGGAGCTTACAGATGAGTGTGCTTCAC 1440
 Db 1440 AGCGAGGAGCTTACAGATGAGTGTGCTTCAC 1440

QY 1440 AGCGAGGAGCTTACAGATGAGTGTGCTTCAC 1440
 Db 1440 AGCGAGGAGCTTACAGATGAGTGTGCTTCAC 1440

QY 1500 TCTTAAAGAACCTTCTGTTGGTCTCTGGAACTTTTAAGTGTGTTGTAAT 1500
 Db 1500 TCTTAAAGAACCTTCTGTTGGTCTCTGGAACTTTTAAGTGTGTTGTAAT 1500

QY 1560 TCTTAAAGAACCTTCTGTTGGTCTCTGGAACTTTTAAGTGTGTTGTAAT 1560
 Db 1560 TCTTAAAGAACCTTCTGTTGGTCTCTGGAACTTTTAAGTGTGTTGTAAT 1560

QY 1560 TCTTAAAGAACCTTCTGTTGGTCTCTGGAACTTTTAAGTGTGTTGTAAT 1560
 Db 1560 TCTTAAAGAACCTTCTGTTGGTCTCTGGAACTTTTAAGTGTGTTGTAAT 1560

RESULT 5

US-10-086-181-6

; Sequence 6, Application US/10086181
 ; Publication No. US20020177151A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GIMENO, Ruth
 ; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF METABOLIC
 ; DISEASES, INCLUDING OBESITY AND DIABETES
 ; FILE REFERENCE: MNI-220
 ; CURRENT APPLICATION NUMBER: US/10/086,181
 ; CURRENT FILING DATE: 2002-02-26
 ; PRIOR APPLICATION NUMBER: 60/271,655
 ; PRIOR FILING DATE: 2001-02-26
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 1086
 ; TYPE: DNA
 ; ORGANISM: Murine ortholog

RESULT 6
; Sequence 14, Application US/10171027
; Publication No. US2003007168A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: 14273 Receptor, A No. US20030073168A1 G-Protein Coupled Receptor
; FILE REFERENCE: MNI-204C03
; CURRENT APPLICATION NUMBER: US/10/171,027
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/456,455
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 181
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-171-027-14

Query Match 11.6%; Score 181; DB 15; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.5e-82;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1021 TGTGGAGTCCTCATCATCACCAACTCTCCATCTGATCAAACCTGGGAGGCC 1080
Db 1 GTGGAGTCCTCATCATCACCAACTCTCCATCTGATCAAACCTGGGAGGCC 60
QY 1081 TGGTCATCTGGCCATCCCTTCTCTGGGGGCGCTTCACCTTGCCAACTCTGCC 1140
Db 61 TGGTCATCTGGCCATCCCTTCTCTGGGGGCGCTTCACCTTGCCAACTCTGCC 120
QY 1141 TAACCCCATATCTGACAATGCGGCGTCAGAACGATGCGGAGATTGCT 1200
Db 121 TAACCCCATATCTGACAATGCGGCGTCAGAACGATGCGGAGATTGCT 180
QY 1201 G 1201
Db 181 G 181
; US-10-171-027-15

RESULT 7
; Sequence 15, Application US/10171027
; Publication No. US20030073168A1
; GENERAL INFORMATION:
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: 14273 Receptor, A No. US20030073168A1 G-Protein Coupled Receptor
; FILE REFERENCE: MNI-204C03
; CURRENT APPLICATION NUMBER: US/10/171,027
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/456,455
; PRIOR FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 138

Query Match 8.8%; Score 138; DB 15; Length 138;
Best Local Similarity 100.0%; Pred. No. 2.3e-60;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 909 AAGAGGCTTACGTTGAGCTTGCGATCTCTGAGAGGCCAGATCCGAGGTGCCCACAA 968
Db 1 AAGAGGCTTACGTTGAGCTTGCGATCTCTGAGAGGCCAGATCCGAGGTGCCCACAA 60
QY 1029 CCCATCATCATCACCATC 1046
Db 121 CCCATCATCATCACCATC 138

RESULT 8
; Sequence 1891, Application US/09535459
; Publication No. US20030040615A1
; GENERAL INFORMATION:
; APPLICANT: Selhamer, Jeffrey J.
; APPLICANT: Delegene, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULES
; FILE REFERENCE: PD-1014 CIP
; CURRENT APPLICATION NUMBER: US/09/535,459
; CURRENT FILING DATE: 2000-03-24
; prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2170
; SOFTWARE: PERL Program
; SEQ ID NO 1891
; LENGTH: 259
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE: NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030040615A1 rat00161335
; NAME/KEY: unsure
; LOCATION: 104, 238
; OTHER INFORMATION: a, t, c, g, or other
; US-09-535-459-1891

Query Match 3.7%; Score 57; DB 10; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.6e-18;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 AGCCTCTTCACTCCAATCTCACAGAACGGGTCATGGAGTGCACACCAGT 74
Db 59 AGCCTCTTCACTCCAATCTCACAGAACGGGTCATGGAGTGCACACCAGT 3

RESULT 9
; Sequence 1891, Application US/09535459
; Publication No. US20030040615A1
; GENERAL INFORMATION:
; APPLICANT: Selhamer, Jeffrey J.
; APPLICANT: Delegene, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULES
; FILE REFERENCE: PD-1014 CIP

CURRENT APPLICATION NUMBER: US/09/535,459
 CURRENT FILING DATE: 2000-03-24 consult PALM or file wrapper
 Prior application data removed - consult PALM or file wrapper
 NUMBER OF SEQ ID NOS: 2170
 SOFTWARE: PERL Program
 SEQ ID NO: 1881
 LENGTH: 261
 TYPE: DNA
 ORGANISM: *Rattus norvegicus*
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No. US20030040615A1 rat00212947
 NAME/KEY: unsure
 LOCATION: 23, 81, 171
 OTHER INFORMATION: a, t, c, g, or other
 US-09-535-459-1881

Query Match 3.7%; Score 57; DB 10; Length 261;
 Best Local Similarity 100.0%; Pred. No. 1.6e-18;
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GCCTCTTCACTCCTCACGAGGGTTCATGGAGTGTACACCATCAGTG 75
 Db 24 GCCTCTTCACTCCTCACGAGGGTTCATGGAGTGTACACCATCAGTG 80

RESULT 10
 US-09-535-459-1892/c
 Publication No. US20030040615A1
 GENERAL INFORMATION:
 APPLICANT: Seilhamer, Jeffrey J.
 APPLICANT: Delegeane, Angelo M.
 APPLICANT: Stuart, Susan G.
 APPLICANT: Stuve, Laura L.
 APPLICANT: Mullany, Sara J.
 APPLICANT: Naughton, Rebecca E.
 TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULE
 FILE REFERENCE: PD-1014 CIP
 CURRENT APPLICATION NUMBER: US/09/535,459
 CURRENT FILING DATE: 2000-03-24
 Prior application data removed - consult PALM or file wrapper
 NUMBER OF SEQ ID NOS: 2170
 SOFTWARE: PERL Program
 SEQ ID NO: 1892
 LENGTH: 285
 TYPE: DNA
 ORGANISM: *Rattus norvegicus*
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No. US20030040615A1 rat00190334
 NAME/KEY: unsure
 LOCATION: 158, 160, 237, 267
 OTHER INFORMATION: a, t, c, g, or other
 US-09-535-459-1892

Query Match 3.7%; Score 57; DB 10; Length 285;
 Best Local Similarity 100.0%; Pred. No. 1.6e-18;
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 AGCTCTTCCACTGCAATCTCACAGAAAGGGGTCTAGGAGTGTACACCATCAGT 74
 Db 107 AGCTCTTCCACTGCAATCTCACAGAAAGGGGTCTAGGAGTGTACACCATCAGT 51

RESULT 11
 US-09-535-459-1882
 Sequence 1882, Application US/09535459
 Publication No. US20030040615A1
 GENERAL INFORMATION:
 APPLICANT: Seilhamer, Jeffrey J.
 APPLICANT: Delegeane, Angelo M.
 APPLICANT: Stuart, Susan G.

RESULT 12
 US-09-535-459-1894/C
 Sequence 1894, Application US/09535459
 Publication No. US20030040615A1
 GENERAL INFORMATION:
 APPLICANT: Seilhamer, Jeffrey J.
 APPLICANT: Delegeane, Angelo M.
 APPLICANT: Stuart, Susan G.
 APPLICANT: Stuve, Laura L.
 APPLICANT: Mullany, Sara J.
 APPLICANT: Naughton, Rebecca E.
 TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULE
 FILE REFERENCE: PD-1014 CIP
 CURRENT APPLICATION NUMBER: US/09/535,459
 CURRENT FILING DATE: 2000-03-24
 Prior application data removed - consult PALM or file wrapper
 NUMBER OF SEQ ID NOS: 2170
 SOFTWARE: PERL Program
 SEQ ID NO: 1894
 LENGTH: 262
 TYPE: DNA
 ORGANISM: *Rattus norvegicus*
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No. US20030040615A1 rat00083975
 NAME/KEY: unsure
 LOCATION: 2
 OTHER INFORMATION: a, t, c, g, or other
 US-09-535-459-1894

Query Match 3.2%; Score 50; DB 10; Length 262;
 Best Local Similarity 100.0%; Pred. No. 6.5e-15;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 119 AGTCGATACCCCTTGTGAGGCCAGGCCAGGCCAGGCCAGGCCAGTTC 168
 Db 110 AGTCGATACCCCTTGTGAGGCCAGGCCAGGCCAGGCCAGTTC 61

RESULT 13
 US-09-535-459-1889/C
 Sequence 1889, Application US/09535459

Publication No. US20030040615A1
; GENERAL INFORMATION:
; APPLICANT: Naughton, Jeffrey J.
; APPLICANT: Deleagane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullaly, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULE
; FILE REFERENCE: PD-101A CIP
; CURRENT APPLICATION NUMBER: US/09/535, 459
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2170
; SOFTWARE: PERL, Program
; SEQ ID NO 1889
; LENGTH: 280
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Incyte ID No. US20030040615A1 rat00204309
; NAME/KEY: unsure
; LOCATION: 20, 230, 260, 268, 273
; OTHER INFORMATION: a, t, c, g, or other
; US-09-535-459-1889
; QUERY Match 2.8%; Score 44; DB 10; Length 280;
; Best Local Similarity 100.0%; Pred. No. 8.2e-12; Mismatches 0; Indels 0; Gaps 0;
; Matches 44; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
; Qy 31 GCACTTCAGAGGGATCTGAGAGCTCACACCATCGT 74
; Db 144 GCAATCTCACAGAGGGCTCAGGAGSTGCTCACACCATCGT 101
; RESULT 14
; US-09-95-225-7
; Sequence 7, Application US/09995225
; Publication No. US20020193584A1
; GENERAL INFORMATION:
; APPLICANT: FEDE, JOHN N.
; APPLICANT: MINTIER, GABE
; APPLICANT: RAMANATHAN, CHANDRA S.
; APPLICANT: HAWKEN, DONALD R.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRM118,
; TITLE OF INVENTION: EXPRESSED HIGHLY IN PITUITARY GLAND AND COLON CARCINOMA
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: D0048NP
; CURRENT APPLICATION NUMBER: US/09/992, 331
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/1308, 540
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/261, 782
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/248, 483
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1086
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-992-331-1
; QUERY Match 2.8%; Score 44; DB 10; Length 1086;
; Best Local Similarity 100.0%; Pred. No. 8.3e-12; Mismatches 0; Indels 0; Gaps 0;
; Matches 44; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
; Qy 852 GGACTGGCATGGATGAGTACTCCAAATTAGATCAC 895
; Db 658 GGACTGGCATGGATGAGTACTCCAAATTAGATCAC 701
; Search completed: October 1, 2004, 04:22:21
; Job time : 733.589 secs